STIC-Biotech/ChemLib



From:

Yaen, Christopher

Sent:

Thursday, August 12, 2004 2:59 PM

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Subject:

09/889300

could you run a regular search and an interference search on seq id 1 and 2

thanks

Christopher Yaen US Patent Office Art Unit 1642 571-272-0838 REM 3A20 REM 3C18



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Type of Search

NA Sequence: #_____

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Structure: #_____

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Vendors and cost where applicable
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U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

Requestor's Name:	Serial Number:	
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August 16, 2004, 11:08:06; Search time 50.4574 Seconds (without alignments) 649.568 Million cell updates/sec
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1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGTLVTVSA 116
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues

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Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1. geneseqD1980s:*
2. geneseqD2000s:*
4. geneseqD2001s:*
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6. geneseqD2001s:*
7. geneseqD2003bs:*
8. geneseqD2003bs:* A Geneseq 29Jan04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Result

Description	Aabl0443 Murine mo	Aaw49814 Amino aci	9	Aar39266 Mouse C4G	Aaw49810 Variable	0	Aae34367 Escherich	Abg71533 Mouse ant	Aar12360 Heavy cha	Aar12238 Mouse MAb	7 ME4	Aaw06216 MAb ME4 h	Aaw85063 Mouse ME4	Abu58897 Mouse ant	Aaw34515 Variable	Aaw49813 Amino aci	Abr55868 Human imm	Aaw07437 Anti-DNA	Aar39267 Humanised	Aaw49817 Fragment	Aar39268 Humanised	Aaw49818 Amino aci	Abr55871 Human imm	Aar43339 Completel	Aaw49816 Amino aci
ПD	AAB10443	AAW49814	ABR55869		AAW49810	8	AAE34367	ABG71533	AAR12360	AAR12238	AAR09427	AAW06216	9	ABU58897	AAW34515	AAW49813	Φ	43	AAR39267	AAW49817	AAR39268	ч	ABR55871	AAR43339	AAW49816
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Abg71534 Mouse ant Aap70624 Sequence			Human	-	Adc65003 Human imm	Aar88716 Mouse ant	Abg71536 Mouse ant	Ade52216 E3Bi prot	Ade52217 pG1EN-EH3	Ade52214 pG1EN-EH3	Aaw00557 Nematode	Aaw43913 Mus muscu	Aaw01585 Lead bind	Aaw00833 Variable
ABG71534 AAP70624	AAW10584 AAW16340	AAW47510	AAW47517 AAW89535	AAB98085	ADC65003	AAR88716	ABG71536	ADE52216	ADE52217	ADE52214	AAW00557	AAW43913	AAW01585	AAW00833
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22.0	7 7 6 6		8 8 8 4	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

s; monoclonal antibody; MAK HE2; heavy chain; variable region; cellular membrane antigen; tumor associated antigen; TAA; vaccine; for Novel use of antibodies against human cellular membrane antigens vaccination against cancer. Murine monoclonal antibody MAK HE2 variable region heavy chain. AAB10443 standard; protein; 116 AA. Example 3; Page 47; 54pp; German. 12-JAN-2000; 2000WO-EP000174. 99CH-00000051. (first entry) Eckert H, Loibner H; (IGEN-) IGENEON GMBH WPI; 2000-475956/41. WO200041722-A1. 13-JAN-1999; 01-DEC-2000 20-JUL-2000. AAB10443; Murine; Mus sp. cancer RESULT 1 AAB10443

This invention describes the novel use of an antibody targeted to a human cellular membrane antigan, to manufacture a medicament to prophylactically and/or therapeutically vaccinate against cancer. The antibodies against tumor associated antigen (TAA) for prophylactic and/or therapeutic vaccination against cancer may be used in low doses (when compared to antibodies against TAA for passive immunotherapy), typically less than 1 mg by injection. The antibodies also have a long continual activity that directly induces immunity and their shelf life is unlimited (fresh vaccination is always possible). This sequence represents the murine monoclonal antibody MAK HEZ variable region heavy chain fragment which is used in the method of the invention

Sequence 116 AA;

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                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
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                                                                                                                                                                                                                                                                                                                                                            Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; caute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                        1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                        QVQLQQSGABLVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                     NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
                                                                                                                                       NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
                             Gaps
                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of the mouse antibody C4G1 mature heavy chain.
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 Length 116;
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100.0%; Score 614; DB 3; Length 1
100.0%; Pred. No. 8e-47;
ive 0; Mismatches 0; Indels
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/note= "complementarity determining
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YAMANOUCHI PHARM CO LID.
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92US-00895952.
92US-00944159.
93US-00059159.
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11-SEP-1992;
03-MAY-1993;
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extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer calls which develop GPIIb/IIIa on their surfaces, for the detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a cell-free, in vitro method of remodeling a peptide. The method involves removing a saccharyl subunit from the peptide, thus forming a truncated glycam, and contacting the truncated glycan with at least one glycosyltransferase and at least one glycosyl to one of the truncated that the truncated glycan thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-GSF) peptide, interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
                                                                                                                                                                                                               1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY
                                                                                                                                                                                           1 QVQLQQSGAELVRPGTSVXVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide remodeling; glycoconjugation; glycosyltransferase; glycan; glycoprotein Ilb/IIIa; monoclonal antibody; human; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-glycoprotein IIb/IIIa MAb mature heavy chain variable region.
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                                                                                                                              90.3%;
91.6%;
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19-OCT-2001; 2001US-0348692P.
2B-NOV-2001; 2001US-0334233P.
2B-NOV-2001; 2001US-0334301P.
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2002US-0404249P.
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                                                                                                                              Query Match
Best Local Similarity
                                                                                                 Sequence 119 AA;
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17-JUL-2002;
16-AUG-2002;
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Factor IX peptide, follicle stimulating hormone peptide, erythropoietin (BPO) peptide, granulocyte macrophage colony stimulating factor (GW-CSF) peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI) peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA) peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-glycoprotein IIb/IIIa moncolonal antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-nody peptide, recombinant DNase peptide, chimeric anti-HER2 antibody peptide, recombinant DNase peptide, inti-TNF alpha peptide, insulin peptide, hepatitis B surface antigen (HbAQ), human growth correct of scanlength attached to the peptide through an intext glycosyl linking is covalently attached to the peptide through an intext glycosyl linking remodeling the above mentioned peptides. The present sequence represents an inti-glycoprotein IIb/IIIa monoclonal antibody mature heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
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|Tabel= signal_peptide
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| Jabel = light_chain
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Best Local Similarity 91.6
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                        Sequence 119 AA;
                                                                                                                                                                                                                                                        variable region
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Gaps

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This is the sequence of the mouse C4G1 immunoglobulin heavy chain. See AAR32265 for the light chain sequence. The antibody is specific for the GPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus useful in the treatment of thrombosis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                   61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                  NEKFKGKATLIYDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWPAYWGRCTLVIVSA 138
                                                                 psn. contg. immunoglobulin specific for the GP-IIB and -IIIA protein treating disorders related to vascular thrombosis.
                                                                                                                                                                                                                                                                                               1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                               20 QVQLQQSGABLVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse, antibody C4G1, heavy chain, humanised, immunoglobulin, Ig, inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction, unstable angina; stroke; transient ischemic episede; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.138
/note= "mature protein"
50.54
/note= "complementarity determining region"
69.065
/note= "complementarity determining region"
                                                                                                                                                                                                                                            Length 138;
                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variable region of mouse antibody C4G1 light chain.
                                                                                                                                                                                                                                         Query Match 90.3%; Score 554.5; DB 2; Best Local Similarity 91.6%; Pred. No. 1.8e-41; Matches 109; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                         Disclosure; Fig 2B; 54pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW49810 standard; protein; 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-00812111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                           WPI; 1993-227275/28.
                                                                                                                                                                                                                 Sequence 138 AA;
                                       N-PSDB; AAQ45663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-1991;
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24-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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Co MS,
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N-PSDB; AAD52608
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                                 cations.
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Region
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                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                      This is the amino acid sequence of the mouse antibody C4G1 heavy chain, used in the method of the invention involving the creation of a humanised immunoglobulin (IG) derived from the mouse C4G1 antibody. The humanised IG is capable of binding to GPIID/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The IG can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acutem myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The IG can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIID/IIIa on their surfaces, for the detection of GPIID/IIIa antigens or for isolating platelets. (Updated on 25-MAR-2003 to correct PA field.)
                                                                         New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                            20 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                        61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                               1 OVOLOOSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                           3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cosmetic;
herbicide;
                                                                                                                                                                                                                                                                                                                      DB 2; Length 138;
                                                                                                                                                                                                                                                                                                                      Score 554.5; DB 2; Length 1
Pred. No. 1.8e-41;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody; Fd fragment; lead cation; perfume; pharmaceutical; health care; skin treatment; pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lead binding MAb 14F11 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW01580 standard, protein; 119 AA
                                                                                                                      Disclosure; Fig 2B; 35pp; English.
(YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murray PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00462798.
95US-00541373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US009258
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.6%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BION-) BIONEBRASKA INC.
                                            WPI; 1998-398136/34.
N-PSDB; AAV36742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wylie DE, Lopez O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-043140/04.
N-PSDB; AAT58254.
                                                                                                                                                                                                                                                                                                 Sequence 138 AA;
                       Co MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9639518-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1996;
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The present sequence represents the heavy chain variable region for monoclonal antibody (MAD) 14F11, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, comedits, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NEKFKCKATLTADKSSSTAYMOLSSLTSDDSAVYFCARDGP---WFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCARSGYGHWYFDVWGAGTTVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.0%; Score 546.5; DB 2; Length 119; 89.9%; Pred. No. 7.7e-41; ive 3; Mismatches 6; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim CS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Song MY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE34367 standard; protein; 138 AA
                                                                                                                                 Claim 12; Page 63; 125pp; English.
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/note= "CDR2"
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/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.99
Watches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31. .35
/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sscherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200292819-A1
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New light and heavy chain variable regions of a monoclonal antibody against the S-surface antigen of the hepatitis B virus (HBV), useful for neutralizing or removing HBV, or for preventing or treating HBV infection.
                                                                                                                                                                            The invention relates to light and heavy chain variable regions of a monoclonal antibody against S-surface antigen of the hepatitis B virus (HBV). The variable regions of the antibodies are useful against HBV S-surface antigens, e.g., adv., adw, ayr or ayw, particularly for neutralising or removing HBV. They may also be employed to treat or prevent HBV. Infection. The present sequence is Escherichia coli heavy
                                                                                                                                    Claim 12; Page 17; 20pp; English.
                                                                                                                                                                                                                                                                                                                        chain variable region
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Sequence 138 AA;

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61 NEKFKGKATLITADKSSTAYMQLSSLTSDDSAVYFCA-----RDGPWFAYWGQGTLVTV 114
                                                                                                             9
                                                                        1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                 1 QVQLQQSGTEMVRPGTSVKVSCKASGYPFTNHLIEWVKQRPGQGPEMIGVINPGSGGTNY
                                                                                                                                                                      61 NEKFKGKATLTADKSSSTAYMQLNSLTSDDSAVYFCAIMTTFLGEGYAMDYWGQGTSVTV
                                          Gaps
84.5%; Score 519; DB 6; Length 138; larity 83.6%; Pred. No. 2.4e-38; Conservative 5; Mismatches 9; Indels
                   Similarity
                                                                                                                                                                                                                                                ss 122
                                                                                                                                                                                                                      SA 116
                                    Matches 102;
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 Query Match
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ABG71533 standard; protein; 164 AA (first entry) 31-DEC-2002 ABG71533; RESULT 8 ABG71533

Mouse; anti-acetyllysine monoclonal antibody; N epsilon-acetyllysine; functional analysis; acetyllysine-containing protein; pathosis; acetylated protein; disease diagnosis; histone acetylation; mab; antibody-producing immortalised cell; heavy chain. Mouse anti-acetyllysine monoclonal antibody (mAb) heavy chain #1

Mus sp.

WO200274962-A1. 26-SEP-2002. 13-MAR-2002; 2002WO-JP002330. 2001JP-00074263. 15-MAR-2001; (NISC-) JAPAN SCI & TECHNOLOGY CORP. (NIHA) JAPAN ENERGY CORP.

Komatsu Y, Yoshida M;

WPI; 2002-750555/81. N-PSDB; ABS55467. Production of anti-acetyllysine monoclonal antibody capable of recognizing Napproximatelyi-acetyllysine regardless of types of adjacent amino acids, useful in e.g. disease diagnosis and searching for novel acetyllysine-containing proteins.

Example 4; Fig 4; 45pp; Japanese

The present invention relates to a mouse anti-acetyllysine monoclonal antibody (mAb) capable of recognising N epsilon-acetyllysine, and a method for producing the monoclonal antibody. The produced antibody is useful in searching for and functional analysis of novel acetyllysine. Containing proteins particularly in studying pathosis due to acetylated proteins, disease diagnosis, facilitating detection of variation in acetylation levels of histone influenced by various stimulations during Western blotting, analysis of the variable region in the DNA sequence of an antibody gene of homology specific to the sequence during the protein translation. The monoclonal antibody of the invention is capable of recognising N epsilon-acetyllysine regardless of the type of adjacent amino acids and accepting adjacent amino acids over a broad range. The present sequence represents a heavy chain of mouse anti-acetyllysine mAb

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Sequence 164 AA;

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                                                                                                                                                                     NEKFKGKATLIADKSSSTAYMQLSSLISDDSAVYFCARD---GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                               QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                            1 OVÓLÓQSGAELVRPGISVKMSCKAAGYTFÍNHWIGWVKORPGHGLEWIGDIYPGSGYTNY
                                               .,
ش
/ Match 84.3%; Score 517.5; DB 5; Length 164; Local Similarity 84.0%; Pred. No. 4e-38; ses 100; Conservative 6; Mismatches 10; Indels 3;
                                                                                                                                                                     61
      Query Match
                            Best Loca
Matches
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Heavy chain variable region of murine 4D12 immunoglobulin. Chimeric antibodies; immunoconjugates; HIV; AIDS Ş AAR12360 standard; protein; 137 (revised)
(first entry) 25-MAR-2003 15-AUG-1991 AAR12360; AAR12360 ID AAR

RESULT

Mus musculus WO9107493-A. 30-MAY-1991.

89US-00433730.

13-NOV-1989;

(XOMA) XOMA CORP. 13-NOV-1989;

Ghoshdasti P, Robinson R; Horwitz AH, Better MD,

WPI; 1991-178105/24. N-PSDB; AAQ12062. New chimeric mouse-human antibodies - used to detect, kill and remove HIV -1 antigen from sample.

Disclosure, Fig 17, 107pp; English.

This is the heavy - chain variable (V) region of a mouse monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 4D12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined

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WPI; 1990-115825/15
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nes 102; Conser
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                                                                                                                                                                                                                                                                                                    Mus musculus.
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04-OCT-1988;
19-JUN-1989;
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Matches
                                                                                                                      AAR09427
                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The mouse VH gene product may be used to produce chimeric mouse- human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in tractment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. See also AAQ12056-61 and AAQ12063. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                   NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                                                                                                                                                                       New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
                                                                                                                                                                               QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                     2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 137;
                                                                                                                          Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
83.9%; Score 515; DB 2;
Best Local Similarity 84.7%; Pred. No. 5.5e-38;
Matches 100; Conservative 4; Mismatches 12;
                                                                                                                          Score 515; DB 2;
Pred. No. 5.5e-38;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ghoshdasti P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 17; 108pp; English.
                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                 AAR12238 standard; protein; 137
                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse MAb 4D12 H chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-00433703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00433703
                                                                                                                          83.9%;
al Similarity 84.7%;
100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GREEN CROSS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Better MD, Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-178106/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZOMA-) ZOMA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ12018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 137 AA;
                                                                                                 Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1; chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
19-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9107494-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-1991.
                                                                                                                                                                                                                                                                                                                                                              AAR12238;
                                                                                                                                                                                                            20
                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

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The sequence is used in the prodn. of a chimeric antibody mol, comprising two light chains and two heavy chains, each having a constant region (funtan) and a variable region (funtine) having specificity to an antigen bound by murine monoclonal antibody (MAb) B38.1. The chimeric antibodies can be used for any purpose for which the original murine MAbs can be body. They are esp. that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constant
20 QVHLQQSGAEMVRPGTSVKVSCRASGYAFINYLIEWVKQRPGGGLEWIGVINPGSGGTTY 79
                                                                               61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                              80 NEKFKDKTTMTADKSSSTAYMHLDSLTSDDSAVYLCARTGSGHALEYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGGGLEWIGVINPGSGDAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes coding for tumour antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 515; DB 2;
Pred. No. 5.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric mouse-human antibodies - prepd. using human region murine variable region, esp. to \bf 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 123 + Fig 30; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen; diagnosis; cancer; tumour.
                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                         ME4 Heavy Chain V Region (mouse).
                                                                                                                                                                                                                                                                AAR09427 standard; protein; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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88US-00253002.
89US-00367641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88US-00241744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-00382768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INT GENETIC ENG INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENETIC
                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horwitz AH,
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AAW85063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU58897
                                                                                                                                                                                                                                                Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
ABU58897
ID ABU58
XX
AC ABU58
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The heavy chain variable region (AAW06216) of mouse monoclonal antibody ME4 is the product of a CDNA clone (AAT43441) isolated from a ME4 hybridoma cDNA library. MAD ME4 (1961) binds to an antigen that is expressed on the surface of human lung, breast, colon and ovary carcinomas and melanomas, but not on most normal adult tissues. The heavy chain and light chain variable regions (see also AAW06219) of ME4 can be linked to human constant regions and expressed in transformed host cells. Novel mouse-human chimeric antibodies (see also AAW06209-14 and AAW06217-18) can the treatment and diagnosis of human cancer. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQSGAELVRPGTSVKVSCTTSGXAFTNYLMEWMKQRPGGGLEWIGVINPGSGDAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                     Chimeric antibody; monoclonal antibody; ME4; antibody engineering; tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma; ovary carcinoma; melanoma; cancer; diagnosis; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 83.9%; Score 515; DB 2; Length 141; al Similarity 85.0%; Pred. No. 5.6e-38; 102; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robinson RR, Horwitz AH;
                                                                                                                                                                               MAb ME4 heavy chain variable region.
                                 AAW06216 standard; protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW85063 standard; protein; 141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 30; 102pp; English.
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88US-00241744.
88US-00243739.
8US-00253002.
89US-00367641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00364001
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                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (XOMA ) XOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1991;
                                                                                                                 25-MAR-2003
13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                    US5576184-A.
                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-SEP-1988
13-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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Matches
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ID AAW8
             AAW0621
                                                     NAMES OF COLOR OF STATES O
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The present sequence represents the heavy chain variable region of murine antibody MAS. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric artibodise also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytotoxifity to purposes in the chimeric antibodies can be used for therapeutic correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NEKFKGKATITADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGQGLEWIGVINPGSGDAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                               Heavy chain variable region; murine antibody ME4; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody; treatment; human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric antibody specific for human tumour antigen - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.9%; Score 515; DB 2;
85.0%; Pred. No. 5.6e-38;
iive 4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoassay, imaging or antitumour agent
                                                                        Mouse ME4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 30; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU58897 standard; protein; 141
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                                                                                                                                                                                                                                                                                                                                                                                                               88US-00240624.

88US-00241744.

88US-00243139.

89US-00357641.

89US-0036768.

89US-00382768.

99US-00059401.

94US-00354001.
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                            (first entry)
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Best Local Similarity 85.0
Matches 102, Conservative
     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Horwitz AH, Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-044574/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV71159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-0CT-1988;
19-JUN-1989;
21-JUL-1989;
06-SEP-1989;
06-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (XOMA ) XOMA
20-MAR-2003
16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
                                                                                                                                                                                                                                                                        US5843685-A.
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                                                                                                                                                                                                                                                                                                                       01-DEC-1998
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Gaps

4 ;

Indels

10;

4; Mismatches

102; Conservative

Matches

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The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen bound by the ING-1 antibody, where the ING-1 is produced by cell line Hobselz as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an important method for detecting an antigen. The antibody is useful in an impel detectable antigen in the sample with the antibody, detecting a label and relating the detected label to the presence of the antigen; to use in an immal by contacting the presence of a label-detectable using the antibody with a part of the antimology cuspected of containing the antigen, detecting the label and relating the cuspected of containing the antigen, detecting the label and relating the cuspected and the presence of the antibody and subjected of containing the antigen, and for killing cells carrying an antigen by contacting the calls with the antibody and allowing the killing to occur. The antibodies are useful in tumour call when the chimeric antibodies bind to the surface of human tumour cells but do not bind detectably to normal cells, e.g., fibroblasts, endothelial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against human the high that these antibodies may mediate selective destruction of antigent contains the major or the antibodies may mediate selective destruction of antigent contains antigent contains
                                                                                                             Mouse, human tumour antigen, anti-human tumour antigen-antibody, ING-1 antibody, cell line HB9812; immunoassay, imaging; tumour diagnosis; tumour therapy, cytostatic; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody.
                                                                   Mouse antibody heavy chain variable region #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 30; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          88US-00240624.
88US-00241744.
88US-00243739.
88US-00253002.
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89WO-US003852.
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94US-00364001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TECHNOLOGY LTD.
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Better MD, Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-196707/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-196707,
N-PSDB; ABK79242
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                                                                                                                                                                                                                                                       US6461824-Bl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XOMA ) XOMA
                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
                        16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-1994;
                                                                                                                                                                                                                                                                                                   08-OCT-2002.
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21-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-1988
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Chang CP;

determinants on the chimeric antibodies increases their resistance to rapid clearance from the body relative to the original murine mAbs. This resistance to clearance enhances the potential utility of these chimeric antibodies, as well as their derivatives, in tumour diagnosis and therapy. This is the amino sequence of a mouse antibody heavy chain variable region used in the creation of an anti-human tumour antigen-

Score 510.5; DB 2; Length 138; Pred. No. 1.4e-37;

83.1%; 84.9%;

Query Match Best Local Similarity

Length 141;

Score 515; DB 6; Pred. No. 5.6e-38;

83.9%;

Query Match Best Local Similarity

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This sequence represents the variable heavy chain of the antibody produced by hybridoma 5-465-210, and can be detected using the method of the produced by hybridoma 5-465-210, and can be detected using the method of antibody which may be present in a test sample. It comprises contacting a test sample suspected of containing the antibody with an antigen specific for the cuspected of containing the antibody with an antigen specific for the engloy the formation of antigen/antibody complexes, detecting the presence of the antibody which may be present in the test sample and employing, as a control or calibrator, a reagent which binds to the antibody constant region epitopes, where the reagent binds to the antigen and is homogeneous with respect to specificity and affinity. The method can be also be used for detecting the presence of antibodies developed against more than one antibodes specific for a given antigen, e.g. HIV-1, hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all of the problems associated with using an immune sera in the manufacture of clandiblay generated in virtually unlimited quantities and are also useful for quantitating, and monitoring the integrity of, the antigen
                                                                     116
                                                                                          9
                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of antibody constant region epitope(s) - as control or calibrator reagents in assays for detecting the presence of an antibody in a test
1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                         20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGQGLEWIGVINPGSGDAKY
                                                                     61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA
                                                                                                                                                                                                                                                                                                                                             Variable region coding sequence; constant region epitope; hybridoma; antibody detection; antigen/antibody complex; variable heavy chain.
                                                                                                                                                                                                                                                                                                          Variable heavy chain of antibody from hybridoma 5-465-210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golden AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 60; 109pp; English.
                                                                                                                                                                                                    AAW34515 standard; protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ostrow DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US001074.
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                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hackett JR, Hoff JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-393833/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT98832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in assays
                                                                                                                                                                                                                                                                           19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9727486-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-1997;
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                                                                                                                                                                                                                                         AAW34515;
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	9	79	116	ď
3; Gaps	SGGTNY	SDFTYY	VTVSA	
3,	VINPG	VINPG	GOGTL	
10; Indels	PGOGLEWIG	PGQGLEWIG	-DGPWFAYW	
10;	SWVKOR	SWVTQR	CAR	
5; Mismatches	KASGYAFTNYLII	KASGYAFTNYLI	DESETSDDSAVY:	
υ, ,,	VKVSC	VKVSC	TAYMO	- A
Matches 101; Conservative	OLOOSGAELVRPGTS	20 QVHLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWYTQRPGQGLEWIGVINPGSDFTYY 79	61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116	80 NEKEKERATUTAN TITLE TO THE TELEVISION T
101;	δ- -	20 02	61 NE	- N
Matches	à	Dp	δ	,C

Search completed: August 16, 2004, 11:12:17 Job time : 51.4574 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - pr	OM protein - protein search, using sw model
Run on:	August 16, 2004, 11:08:06 ; Search time 46.5426 Seconds (without alignments) 649.568 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-889-300A-2 562 1 NIVMTQSPKSMSMSVGERVTCGQGYSYPYTFGGGTKLEIK 107
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1586107 segs, 282547505 residues Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	Aaw47086 Mouse U59	4 J591 mono	ın	Aabl0444 Murine mo	Aar27144 1E6 kappa	Aaw47085 Mouse J59	Aay90370 J591 mono	C)	ıŋ	Abq74248 Mouse ant	2	m	9	Aaw01632 Ber-H2 he	Aay71545 Mouse AF2	3	Aaw00828 Variable	Abol0727 Variable	Abr44618 Murine J4	Abr44671 Murine J4	Abol0737 Variable	Abol0738 Variable	Abr44682 Murine J4	Abr44624 Murine J4	Abr44622 Murine J4	
SUMMARIES	AAW47086	AAY90374	AAB36225	AAB10444	AAR27144	AAW47085	AAY90370	2	AAW01145	ABG74248	ABR82783	ABR82893	ABB07176	AAW01632	AAY71545	AAB69693	AAW00828	ABO10727	ABR44618	ABR44671	ABO10737	ABO10738	ABR44682	ABR44624	ABR44622	
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ery tch	100.0	00	00	\circ	100.0	8	8	0	0	\circ	100.0	O	S	3	2	(1)	0	9	9	σ	~	~	87.2	~	^	
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- o n		Abr44621 Murine J4 Abo10741 Consensus Abo10729 Variable Abo10740 Variable		AD744885 MULILIE 04 AD744617 MULINE 04 AD744673 MULINE 04 AA764812 SCFV anti	Abol0735 Variable Abr44620 Murine J4 Abr44679 Murine J4
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ALIGNMENTS

RESULT 1

Mouse, monoclonal antibody, JS91; prostate specific membrane antigen; cancer; vascular endothelial cell; metastatic adenocarcinoma. Mouse J591 monoclonal antibody light chain variable region. Ä AAW47086 standard; protein; 107 (CORR) CORNELL RES FOUND INC. 97WO-US012035. 96US-0022125P. 97US-00838682. (first entry) WPI; 1998-120937/11. N-PSDB; AAV13952 WO9803873-A1. 26-JUN-1998 17-JUL-1997; 18-JUL-1996; 09-APR-1997; 29-JAN-1998. Bander NH; AAW47086; Mus sp. AAW4708

6 Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or normal, hypertrophic or cancerous prostatic cells, also used for diagnosis.

Example 12; Page 60; 94pp; English.

The present sequence represents the mouse U591 monoclonal antibody light chain variable region from an example of the present invention. The present invention describes the elimination of cancer cells by treating vascular endothelial cells (UEC) close to the cancer with an agent (A) able to bind to the extracellular domain (ECD) of prostate specific membrane antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the detection of cancer tissue by detecting binding of labelled (A) to VEC (Dese to, or within, a cancer cancer cancer published are concerting by electing or detecting or membrane and cancer cancer cancer cancer cancer cancer cancer cancer cancer prostate epithelial cells using optionally labelled (A); (3)

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The method is used to treat renal, urothelial, colon, lung, rectal or bleast cancers and metastatic adenocarcinoms of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cancer (presence of PSMA in the serum indicates that prostate cells are being lysed). (A) binds to an epitope of PSMA expressed on live cells (contrast antibody 7E1 which only binds after cell lysis), allowing targeting of live, unfixed cells and thus providing more efficient treatment and diagnosis. Both cancer cells themselves and the VEC on which they depend are killed. All VEC close to cancer cells express PSMA, whatever the type of cancer, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is a fragment of the light chain of the monoclonal antibody U591. The invention relates to an isolated antibody or its antigen binding portion (I) which binds to an extracellular domain of prostate specific membrane antigen and which does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells. (I) is useful for diagnosis of diseases associated with the presence of normal, benign
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hybridomas that produce a monoclonal antibody (MAb) that binds to PSMA.
                                                                                                                                                                                                                                                                                                                                                                                       1 NIVMIQSPKSMSMSVGERVTLICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or normal, hypertrophic or cancerous prostatic cells, also used for
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J591 monoclonal antibody, extracellular domain, diagnosis, therapy, prostate specific membrane antigen, prostate cancer, light chain.
                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J591 monoclonal antibody light chain protein sequence fragment.
                                                                                                                                                                                                                                                                                    100.0%; Score 562; DB 2; Length 107; 100.0%; Pred. No. 4.1e-39; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFTGSGSATDFTLTISSVQAEDLADYHCGGGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK
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96US-0022125P.
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Best Local Similarity 100.
Matches 107; Conservative
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                                                                                                                                                                                                             normal VEC do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA37834.
                                                                                                                                                                                                                                                   Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-1996;
18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2001
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hyperplastic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when the disease is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used alone or bound to a substance effective to kill cancerous prostate epithelial cells as a therapy for prostate cancer. Binding and internalising of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cytotoxic agents. (I) targets only prostate epithelial cells and other tissue are spared which provides safer treatment particularly for elderly patients. The antibodies bind to living prostate cells and treatments using these antibodies are more effective than those which target lysed prostate
                                                                                                                                                                                                                                                                                                                                                                               1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or on
                                                                                                                                                                                                                                                                                                                                                                                                                 1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, cnormal, hypertrophic or cancerous prostatic cells, also used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; antibody; heavy chain; prostate cancer; biological agent.
                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody J591 kappa light chain V region #1.
                                                                                                                                                                                                                                                                                                      100.0%; Score 562; DB 2;
100.0%; Pred. No. 4.1e-39;
ive 0; Mismatches 0;
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96US-0022125P.
97US-00838682.
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                                                                                                                                                                                                                                                                                                                          Local Similarity ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-120937/11.
N-PSDB; AAC66544.
                                                                                                                                                                                                                                                                      Sequence 107 AA;
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NIVMTOSPKSMSWGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the novel use of an antibody targeted to a human callular membrane antigen, to manufacture a medicament to prophylactically and/or therapeutically vaccinate against cancer. The antibodies against tumor associated antigen (TPA) for prophylactic and/or therapeutic vaccination against cancer may be used in low doses (when compared to antibodies against TPA for passive immunotherapy), typically less than 1 mg by injection. The antibodies also have a long continual activity that directly induces immunity and their shelf life is unlimited firesh waccination is always possible). This sequence represents the which is used in the method of the invention
                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                   Murine, monoclonal antibody, MAK HE2, light chain, variable region, human cellular membrane antigen, tumor associated antigen, TAA, vaccine,
an antibody which may be used as the biological agent of the invention. In addition to prostate cancer, the method can be used with renal, urothelial, colon, renal, lung and breast cancer cells, and cancerous cells of metastatic adenocarcinoma to the liver
                                                                                                                                                1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                             1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel use of antibodies against human cellular membrane antigens for
                                                                                                      ..
                                                                                                                                                                                                                                                                                                                           Murine monoclonal antibody MAK HE2 variable region light chain.
                                                                                                                                                                                        61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                          61 RFIGSGSAIDFILIISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                Length 107;
                                                                                                     0; Indels
                                                                              100.0%; Score 562; DB 2;
100.0%; Pred. No. 4.1e-39;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 47-48; 54pp; German.
                                                                                                                                                                                                                                                          AAB10444 standard; protein; 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccination against cancer.
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                         Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loibner H;
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                                                        Sequence 107 AA;
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NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric; heavy chain; variable region; monoclonal antibody; lymphocyte function associated antigen-3; LFA-3; inflammation; autoimmune disease; immunomodulation; systemic lupus erythematosus;
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100.0%; Score 562; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.2e-39;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1E6 kappa light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis, thyroiditis.
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89. .97
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                                                                                                                                                                                                                                                                                                                                                                               (revised)
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20-MAY-1998
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107; Conservative
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Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse, monoclonal antibody, J591, prostate specific membrane antigen, cancer, vascular endothelial cell, metastatic adenocarcinoma.
                                                                                                                                                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse J591 monoclonal antibody light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                          AAW47085 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0022125P.
97US-00838682.
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N-PSDB; AAV13951.
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09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW47085;
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This sequence is the kappa light chain of the monoclonal antibody U591.

The invention relates to an isolated antibody or its antigen binding portion (I) which bind does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells (I) is useful for diagnosis of diseases associated with the presence of normal, benign hyperplatic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when the disease is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used patient for e.g. recurrence of prostate concer. They can also be used epithelial cells as a therapy for prostate cancer. Binding and internalishing of the antibody with the prostate specific membrane antiem, permits the therapeutic use of intracellularly acting cyclotoxic apents. (I) targets only prostate epithelial cells and other tissue are spared which provides after readment particularly for elderly patients. The antibodies are more effective than those which target lysed prostate entitled.
                                      1 NIVMIQSPKSMSMSVGERVTLICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                               7 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                       J591 monoclonal antibody; extracellular domain; diagnosis; therapy; prostate specific membrane antigen; prostate cancer; kappa light chain.
  Gaps
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                                                                                                                    61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
  Indels
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  Mismatches
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96US-0022125P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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18-JUL-1996;
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DB 2; Length 121;

100.0%; Score 562;

Query Match

Score 562; DB 2; Length 121; Pred. No. 4.7e-39;

100.0%;

Query Match Best Local Similarity

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Matches

엄 ò 임 AAB36222;

AAB36222

Mus sp.

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Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, crebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and collitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma B3U1 (PASSARAB.U) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture eupernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CLAB. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly
                                                                                                                                                                                                                                                                             Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis; cerebral infarction; acute Kidney failure; colitis; chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing disease; hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody inhibiting type II phospholipase A2 activity - for treatment of myocardial and cerebral infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 NIVMTQSFKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNKYTGVPD
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                                                                                                                                                                                                                                        MAb 10.1 light chain, directed against type II phospholipase A2.
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                 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
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100.0%; Pred. No. 4.9e-39;
iive 0; Mismatches 0;
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                                                                                                                  AAW01145 standard; protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 13; 69pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                44. .54
/label= CDR 1
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/label= CDR 3
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/label= CDR
                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 107; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawauchi Y,
                                                                                                                                                                                                   10-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                 67
                                                                                                  AAW01145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method of killing cancer cells, particularly prostate cancer cells, by directing a biological agent to the cells which then binds to a prostate specific membrane antigen and causes the molecule to be internalised. The internalisation of the agent, which may be bound to a drug or which may act to kill the cell alone, then leads to the death of the cell. The present sequence forms part of an antibody which may be used as the biological agent of the invention. In addition to prostate cancer, the method can be used with renal, urchhelial, colon, renal, lung and breast cancer cells, and cancerous cells of metastatic adenocarcinoma to the liver
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                                                                                                             7 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for
                                                                         1 NIVMTQSPKSMSWGERVTLICKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                61 RFTGSGSATDFTLTISSVQAEDLADYHCGGGSYRYTFGGGTKLEIK 107
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61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK
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                                                                                                                                                                                                                                                                                                                                                                                                                        Murine monoclonal antibody J591 kappa light chain #1.
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100.0%; Pred. No. 4.7e-39;
tive 0; Mismatches 0;
                                  Mismatches
                 Pred. No.
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96US-0022125P.
97US-00838682.
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               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                  Conservative
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            Local Similarity
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diagnosis.

Query Match Local

Best Loca Matches

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18-DEC-2003 (first entry)
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                                                                                                                                                                                                         Homo sapiens.
                                                                                          18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a chimaeric molecule comprising the GD3

(ganglioside antigen) binding domain of antibody MB3.6, with any of 3

variable gene sequences, or the PSMA (prostate-specific membrane antigen)

binding domain of antibody 3D8, 4D4 and 3B11, with variable gene

be equences, the zeta signalling chain of the T cell receptor and an

intervening CD8alpha hinge in which cysteine residues have been mutated.

The chimaeric molecules expressed in T cells or NK cells or other

effector cells are useful in treating patients with cancers expressing

the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3B11 derivatives),

and/or together with each other or with heterologous constructs to engage
additional stimulatory and functional properties of the effector cells to

enhance the antitumour therapeutic efficacy (claimed). They are

tumours and prostate and small cell lung cancer. The present sequence

tumours and prostate and small cell lung cancer. The present sequence

represents the mouse antibody 3B11 light chain variable region
                                                                                                                                                                                                     T-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; PSVA; tumour; 3D8; 4D4; BI1; prostate-specific membrane antigen; zeta signalling chain; CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; light chain variable region; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.
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                                                                                                                                                                    Mouse antibody 3E11 light chain variable region.
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                                                         ABG74248 standard; protein; 132
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                                                                                                                              (first entry)
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Best Local Similarity 100.
Matches 107; Conservative
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                                                                                                                                  22-APR-2003
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                                                                                            ABG74248;
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The invention relates to treating a human patient diagnosed with a B-cell malignancy. The method involves (a) administering to the human patient a blocking anti-CD22 monoclonal antibody binding to the first two 1g-like domains, or to an epitope within the first two Ig-like domains of native human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the mailgrancy to the treatment. The method is useful for treating a human patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma, Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy cell leukemia or prolymphocytic leukemia. The present sequence represents the amino acid sequence for kappa light chain V-J junction for anti-CD22 antibody from hybridoma HB22-196
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                                                                                                                                                                                                                                                                                                       CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating a human patient diagnosed with a B-cell malignancy by administering a blocking anti-CD22 monoclonal antibody binding to the first two Ig-like domains of native human CD22 (hCD22).
                                                                                                                                                                                                                                Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
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100.0%; Pred. No. 5.2e-39;
iive 0; Mismatches 0;
ABR82783 standard; protein; 135 AA.
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21-OCT-2002; 2002US-0420472P.
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(REGC ) UNIV CALIFORNIA.
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The invention provides a neuromodulatory agent (1) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting ca2+ signaling with oligodendrocytes. An humanised antibody to (1) can be selected from antibody sHigM22 (LMM 22), ebvHigM Ms19D10, ebv HigM comparison of CNS axons, or treating demyelinating proliferation of glial cells in need of such therapy. (I) is capable of binding to structures and cells within CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TME) or for treating a human being having multiple sclerosis, or a human or domestic animal with a viral demyelinating disease, or a post-neural disease of CNS. (I) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for stimulating remyelination of CNS axons. The antibodies are useful for preventing infection by a bacterium, virus or like to pathodes that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the mouse 09 antibody kappa light chain l variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                        neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious
                                                                                                                                                                                                                                                (MAYO-) MAYO FOUND MEDICAL EDUCATION RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 35A-B; 219pp; English.
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                                                                                                                                   30-MAY-2000; 2000WO-US014902
                                                                                                                                                                                           10-MAY-2000; 2000US-00568351.
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                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-066596/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encephalomyelitis
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                          WO200185797-A1.
                                                                                 15-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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AC AAW0
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DT 22-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to treating a human patient diagnosed with an autoimmune disease. The method involves administering to the patient an amount of a blocking anti-CD22 monoclonal antibody and monitoring the response of the autoimmune disease to the treatment. The method is useful in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis, lashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The present sequence represents the amino acid sequence for kappa light chain V-J junction for anti-CD22 antibody from hybridoma HB22-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating an autoimmune disease or a B-cell malignancy in a human patient comprises administering an amount of an anti-CD22 monoclonal antibody to the patient and monitoring the response of the disease to the treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80
                                                                      CD22; autoimmune disease; anti-CD22 antibody; ilmmunosuppressive; cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer; antiarthritic; antipscriatic; thyromimetic; antianemic; antidiabetic; antiallergic; gene therapy; HB22-196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                       Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse 09 antibody kappa light chain 1 variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 562; DB 7;
100.0%; Pred. No. 5.2e-39;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB07176 standard; protein; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 23; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002; 2002US-0359419P.
21-OCT-2002; 2002US-0420472P.
                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2003; 2003WO-US005549
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107; Conservative
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                                                                                                                                                                                                                                                                       WO2003072736-A2
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               redder TF;
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RESULT 13 ABB07176

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                                                                                                                                                                    1 NIVWIQSPKSMSMSVGBRVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
                                                               0; Gaps
95.0%; Score 534; DB 5; Length 101; 100.0%; Pred. No. 8e-37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        61 RFIGSGSATDFILTISSVQAEDLADYHCGQGYSYPYTFGGG 101
                                                                                                                                                                                                                                                                                                              RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGG 101
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Search completed: August 16, 2004, 11:12:18 Job time : 47.5426 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The ligands are useful for diagnosis or therapy of CD30 expressing cancers, esp. Hodgkinson's disease. Cytoplasmic RNA was isolated from calls of the mouse myeloma hybrid line Ber-H2. CDNA was isolated using reverse transcriptase. A VHDJ fragment contg. band was cut from a gel and purified. DNA corresponding to VK and Vgamma was isolated and cloned into vectors. Oligonucleotides used are given in AAT58331 to AAT58340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised antibody, HuZAF; mouse AF2 antibody, human EU antibody, AF2-VL; light chain variable region; VL; heavy chain variable region; VH; 1gG2b; gamma-interferon; IFN; complementarity determining region; CDR; FR; framework region; immunosuppressive; antihiflammatory; antisclerotic; gastrointestinal; antidiabetic; antiarthritic; dermalogical; inhibitor; mutoimnume disease; graft versus host disease; organ transplant; multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis; systemic lupus erythematosus; SLE; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                       DNA mols. encoding CD30-specific immunoglobulin variable regions - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 NIVMTQSPRSMSMSVGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
             immunoglobulin; variable region; CDR; cancer; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NIVMTQSPKSMSMSVGERVTLFCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 527; DB 2; Length 136;
Pred. No. 4.1e-36;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse AF2 antibody light chain variable region (AF2-VL).
                                                                                                                                                                                                                                                                                       (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.
                                                                                                  1. .29
/label= sig_peptide
                                                                                                                                           /label= mat_protein
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY71545 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 15; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                         cancer diagnosis or therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.8%;
94.4%;
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                                                                                                                                                                                                                                                                                                                   Ziegler A, Stein H;
                                                                                                                                                                                                                                                                                                                                                WPI; 1996-507017/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT58329
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                                                                                                                                                                        DE19543039-C1
                                                         Homo sapiens.
                                                                                                                                                                                                                                                            08-NOV-1995;
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                                                                                                                                                                                                  21-NOV-1996.
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Best Local S
                                                                                                  Peptide
                                                                                                                                 Protein
                            Ber-H2
                CD30;
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The present amino acid sequence is the mouse AF2 antibody, light chain variable region (AF2-VL). It has IgG2b isotype and kappa light chain. It is used for the construction of humanised version of mouse AF2 antibody HuZAF, that comprises mouse antibody AF2 complementarity determining regions (CDRs), functionally joined to the human acceptor antibody EU framework region (FR). HuZAF antibody specifically binds to and neutralises gamma-interferon (IFN). They can also block the binding of mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences that are immunogenically active in humans and remains unaffected by immune responses, that may reduce its activity or circulating half-life. HuZAF may be administered to treat autoimmune diseases such as graft versus host disease following organ transplant, Type I diabetes, multiple sclenes, rehumatoid arthritis, psoriasis, systemic lupus erythematosus (SLE), Habimcto's thyroiditis, pirmary biliary cirrhosis and inflammatory bowel disease like, Crohn's disease
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                                                                                                                 /note= "Mature mouse antibody AF2 light chain variable region (AF2-VL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWXQQKPEQSPKLLIYGASNRYTGVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-interferon for the treatment of autoimmune diseases, e.g. multiple sclerosis and diabetes,
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                                                                                                                                                                                                                                                                       70. .76
/label= CDR
/note= "Complementarity determining region"
1109. .117
/label= CDR
/note= "Complementarity determining region"
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                                                                                                                                                                                      44. .54
|abel= CDR
'note= "Complementarity determining region"
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Pred. No. 1.2e-35;
5; Mismatches 4;
                                                             note= "N-terminal peptide"
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iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1A; 32pp; English.
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1 Similarity 91.6%;
98; Conservative
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                                                                                              .127
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200032634-A1
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Sequence 103, App
Sequence 103, App
Sequence 103, App
Sequence 103, App
Sequence 4, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 25, Appl
Sequence 18, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
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100.0%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.4e-50;
Matches 107; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGS-08-838-682-16
Sequence 16, Application US/08838682
Sequence 16, Application US/08838682
Sequence 16, Application US/08838682
Sequence 16, Application US/08838682
SEQUENCE OF INVENTION:
APPLICANT: Bander M.D., Neil H.
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle Lip
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,682
FILING DATE:
CLASSIFICATION = 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-WAY-1996
PRIOR APPLICATION DATE: US 60/012,125
FILING DATE: 18-JUL-1996
ATTONNUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
ATTONENYAGENT INFORMATION:
APPLICATION NUMBER: 30,727
REFRENCE/DOCKET NUMBER: 30,727
REFRENCE/DOCKET NUMBER: 30,727
REFRENCE/DOCKET NUMBER: 19603/1172
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 16:
SEQUENCE CHRRACTERISTICS:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHRRACTERISTICS:
LENTH: 10.7 main a acids
   US-07-634-278-103
US-08-477-728-103
US-08-474-040-103
US-08-487-200-103
US-08-4857-1103
US-08-450-520h-6
US-09-1177-370-4
US-09-118-25
US-09-118-25
US-09-118-25
US-09-118-118-25
US-09-118-118-25
US-09-118-118-118
US-08-253-8776-55
US-09-253-8776-55
US-08-253-8776-55
US-08-253-8776-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rochester STATE; New York COUNTRY: U.S.A. ZONTRY: U.S.A. ZONTRY: U.S.A. ZONFUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIDIE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS:
       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-682-16
       Appliant App
                                                                                                                                                                                                                              August 16, 2004, 11:08:07; Search time 13:9148 Seconds (without alignments) 396.986 Million cell updates/sec
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/FUTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-835-914-16
US-09-357-707-16
US-09-357-707-16
US-08-895-914-11
US-08-895-914-11
US-09-377-710A-11
US-09-377-710A-11
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US-09-377-710A-11
US-09-377-710A-11
US-09-377-710A-11
US-09-377-710A-12
US-08-444-59-99
US-08-444-59-99
US-08-554-840-4
US-08-55-339-4
US-08-55-339-4
US-08-55-339-2
US-08-32-339-2
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US-08-32-339-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                            1 NIVWIQSPKSMSVGERVTLICKASENVVTVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
1 NIVMIQSPKSMSMSVGERVILITCKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
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                                                                                                                  100.0%; Score 562; DB 3; Length 107; 100.0%; Pred. No. 3.4e-50;
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                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
CITY: Rochester Clinton Square, P.O. Box 1051
CITY: Rochester Clinton Square, P.O. Box 1051
CITY: Rochester Clinton Square, P.O. Box 1051
COUNTY: U.S.A.
ZIP: 14603-1051
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
COMPUTER: BM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
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CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-UUL-1996
PRIOR APPLICATION NUMBER: US 08/838,682
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERENCE/DOCKET NUMBER: 19603/1173
TELECOMMUNICATION INPORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                Sequence 16, Application US/08895914 Patent No. 6136311 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (716) 263-130
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
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amino acid
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Best Local Similarity 100.
Matches 107; Conservative
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                                                    GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TILLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
TILLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REPRENCE: Lois M. Kwasigroch: BZL 242/025
CURRENT PAPLICATION NUMBER: US/09/357,710A
CURRENT PAPLICATION NUMBER: US/09/357,710A
PRIOR FILING DATE: 1999-07-20
PRIOR PAPLICATION NUMBER: US/00/06,976
PRIOR PILING DATE: 1996-05-06
PRIOR PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
LENGTH: LOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BUNGERATION: TREATMENT AND DIAGNOSIS OF CANCER TILLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER FILE REPERENCE: Lois M. Kwasigroch: BZL 242/078 CURRENT APPLICATION NUMBER: US/09/357,707 CURRENT PILLICATION NUMBER: US 08/895,914 PRIOR APPLICATION NUMBER: US 08/898,682 PRIOR FILLING DATE: 1997-07-17 PRIOR PAPLICATION NUMBER: US 08/838,682 PRIOR FILLING DATE: 1997-04-09 PRIOR FILLING DATE: 1996-05-06 PRIOR FILLING DATE: 1996-05-06 PRIOR FILLING DATE: 1996-07-18 NUMBER: US 60/022,125 PRIOR FILLING DATE: 1996-07-18 NUMBER: PARCHAIN DATE: 1996-07-18 NUMBER: PARCHAIN DATE: 1996-07-18 NUMBER: PARCHAIN VERSION 3.0 SEQ ID NOS: 21 SEQ ID NOS: 21
Sequence 16, Application US/09357710A Patent No. 6290956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-357-707-16; Sequence 16, Application US/09357707; Sequence 16, Application US/09357707; Patent No. 6649163; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Mus sp. US-09-357-710A-16
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1 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD
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Sequence 11. Application US/08895914;
Fatest No. 613631
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
APPLICANT: BANDER: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603-1051
COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
FILING DATE: CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 562; DB 3;
100.0%; Pred. No. 3.9e-50;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 121 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 107; Conservative
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MOLECULE TYPE: protein
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      General Name of Application PC/TUS9202044
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: BIOGEN, INC.
APPLICANT: CHISHOLM Patricia L.
APPLICANT: WALLINER, BATCHAR P.
TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: G/O FIGH & NEAVE
STREET: 875 Third Avenue
CITY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 562; DB 5; Length 109; 100.0%; Pred. No. 3.5e-50; tive 0; Mismatches 0; Indels
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Patent No. 6107090
GENERAL INFORMATION:
APPLICANT: BANDER OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESSEE: NIXON, HARGIAVE, DEVANS & DOYLE LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSINING DATE: 19920312
CLASSIPICATION NUMBER: US 07/667,975
FILING DATE: 19920312
CLASSIPICATION NUMBER: US 07/667,975
FILING DATE: 12-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REPERENCE/POCKET NUMBER: B150CIP
TELEPHONE: (212) 715-0600
TELEPHONE: (212) 715-0600
TELEFREX: (212) 715-0600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 109 amino acids
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Matches 107; Conservative
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RESULT 5
PCT-US92-02044-2
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99

Gaps

0

Indels

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Length 121;
           COUNTRY: New York
COUNTRY: U.S.A.
2IP: 14603-1031
COMPUTER: ENABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENABABLE FORM:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
SURPRARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/838,682
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/976
FILING DATE: US/MA-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/022,125
FILING DATE: US/UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: GOLIAman, MICHABLE US/UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: GOLIAMAN, MICHABLE US/UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: GOLIAMAN, MICHABLE US/UL-1996
ATTORNEY/AGENT INFORMATION:
TELEFRANCE/DOCKET NUMBER: 19603/1172
Rochester
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21 NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80
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Best Local Similarity 91.61
Matches 98; Conservative
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US-09-450-520A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus sp.
                                               JS-09-357-707-11
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Sequence 11, Application US/09357710A
Patent No. 629056
GENERAL INFORMATION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: Lois M. Kassigroch: BZL 242/025
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US/09/357,710A
PRIOR PLING DATE: 1999-07-20
PRIOR PLING DATE: 1996-07-06
PRIOR PLING DATE: 1996-07-06
PRIOR PLING DATE: 1996-07-18
NUMBER: US 60/016,976
PRIOR PLING DATE: 1996-07-18
NUMBER: US 60/022,125
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
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100.0%; Pred. No. 3.9e-50;
ive 0; Mismatches 0;
            FILING DATE: 06-MAY 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/022,125

FILING DATE: 18-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/838,682

FILING DATE: 09-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: GOLdman, Michael L.

REGISTRATION NUMBER: 30,727

REFERENCE/DOCKET NUMBER: 19603/1173

TELEPHONE: (716) 263-1600

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: Amino acids
APPLICATION NUMBER: US 60/016,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 107; Conservative
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US-09-357-710A-11
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APPLICANT: Landolfi, Nicholas F.
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Naoya
APPLICANT: Queen, Cary L.
APPLICANT: Queen, Cary L.
APPLICANT: Procein Design Labs, Inc.
TILE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-00811003
CURRENT APPLICATION NUMBER: US/09/450,520A
CURRENT FILING DATE: 1999-11-29
PRIOR PAPLICATION NUMBER: 60/110,523
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
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Pred. No. 6.2e-46;
5; Mismatches 4; Indels
                                                                             JAPPLICANT: BANGER, Neil H.

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER

FILE REPERENCE: Lois M. Kwaasigroch: BZL 242/078

CURRENT APPLICATION NUMBER: US/09/357,707

CURRENT FILING DATE: 1999-07-20

FRIOR FILING DATE: 1999-07-17

FRIOR APPLICATION NUMBER: US 08/838,682

FRIOR APPLICATION NUMBER: US 60/016,976

FRIOR APPLICATION NUMBER: US 60/016,976

FRIOR APPLICATION NUMBER: US 60/02,125

FRIOR APPLICATION NUMBER: US 60/022,125

FRIOR APPLICATION NUMBER: 1996-07-18

NUMBER OF SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NO 11
Sequence 11, Application US/09357707; Patent No. 6649163
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09450520A
Patent No. 6329511
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                                                                                                                   Sequence 99, Application US/07634278
; Sequence 99, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: OUBEN, Cary L.
APPLICANT: OCHAIDER, William P.
APPLICANT: SCHNEIDER, William P.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: CALNEOLER, William P.
; APPLICANT: CALNEOLER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
CITY: Palo Alto
STRATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                          81 RFTGSGSATDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 127
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Pred. No. 6.8e-46;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTE: 7430.

COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATURG-SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION NUMBER: US/07/634,274
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATPONNY/AGENT INPOMMATION:
NAME: CAMPTH MAILTING DATE: 28-DEC-1988
ATPONNY/AGENT INPOMMATION:
NAME: CAMPTH MAILTING DATE: AMARENEENT NUMBERS OF CAMPTH MAILTING DATE: AMARENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 11823
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.78;
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amino acid
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Best Local Similarity 91.6
Matches 98; Conservative
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RESULT 12

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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Sequence 99 Stabblication US/08477728

Sequence 95 Stabblication US/08477728

Serient No. 5585089

GENERAL INFORMATION:
APPLICANT: OUEN, William P.
APPLICANT: SELICK, Harold E.
TILLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSED: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
CONDUTER: ISM PC compatible
OCMUNTR: ISM PC compatible
COMPUTER: ISM PC compatible
CLASSIFICATION NUMBER: US/88 477,728
FILING DATE: NAME
CLASSIFICATION NAME
CLASSIFICATION NAME
PD PD ROW NAME
PD PD ROW NAME
PD POLICATION NAME
PD POLICA
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Pred. No. 6.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

FILING DATE: 13-FEB-1989

FILING DATE: 128-DEC-1988

APPLICATION NUMBER: US 07/290,975

FILING DATE: 128-DEC-1988

ATORNEY/AGENT INFORMATION:
NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 11823-00260

TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 99, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION: APPLICANT: QUEEN, Cary L. APPLICANT: CO, Man Sung APPLICANT: SCHNEIDER, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QUEEN, Cary L.
CO, Man Sung
SCHNEIDER, William P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.7%;
91.6%;
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amino acid
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Best Local Similarity 91.6'
Matches 98; Conservative
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US-08-474-040-99
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us-09-889-300a-2.rai

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1 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
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US-08-484-537-99
Sequence 99, Application US/08484537
Fatent No. 6180370
Fatent No. 6180370
Fatent No. 6180370
FAPPLICANT: QUEEN, Cary L.
APPLICANT: GO, Man Sung
APPLICANT: COLNEIDER, William P.
APPLICANT: COLINGH, Kathleen L.
APPLICANT: SELICK, Harcld E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COMPANIANT CONTROL OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COMPANIANT CONTROL OF COURTS ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TRANSPORTER: TOWN-1905
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-DEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/200,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, WILLIAM M
REGISTRATION NUMBER: 11823-002610
TELECOMMUNICATION NUMBER: 11823-002610
TELECOMMUNICATION NUMBER: 118023-002610
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 136 amino acids
amino acid
3Y: linear
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Best Local Similarity 91.6'
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-487-200-99
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
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Fatent No. 5693762
Fatent No. 5693762
Fatent No. 5693762
Fatent No. 5693762
Fatent No. 6993762
Fatent No. 6993762
Fatent Cary L.
Fatent Cary Co. Man Sung
Fatent Cary Cary Co. Man Sung
Fatent Cary Co. Man Sung

                                APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGELOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTE: IBM PC compatible
CONFURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
NAMME: SMICH, William M
REGISTRATION NUMBER: 11823-002600
TELECOMMUNICATION NUMBER: 11823-02600
TELECOMMUNICATION NUMBER: 11823-02600
                                                                                                                                                                                                                                                                                                      STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 136 amino acids
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US-08-487-200-99
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us-09-889-300a-2.rai
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STATE: COUNTY: US

STATE: COUNTY: US

The 9401 COUNTY: US

COUNTY: US

CONFUTER READALE FORM:

MODION TYPE: Flopy disk

CONFUTER: Tab FC compatible

CONFUTER: Tab FC compatible

CONFUTER: Tab CONFUTER: Tab FC compatible

CONFUTER: Tab CONFUTER: US conf
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Sequence 16, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 19, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 34, Appl
Sequence 2, Appli
Sequence 84, Appl
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864.269 Million cell updates/sec
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                                                                                                                                                                                                                                              562
1 NIVMTQSPKSMSWGERVT......CGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                August 16, 2004, 11:10:36; Search time 38.8655 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

| cgn2_6/ptdata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptdata/2/pubpaa/USO6_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-929-546-16

US-09-929-546-11

US-09-929-546-11

US-10-010-729-70

US-10-010-729-70

US-10-372-481-31

US-10-371-797-31

US-08-779-784-34

US-09-928-54-2

US-10-310-729-21

US-09-928-54-2

US-10-389-417-84

US-10-389-417-84

US-10-389-417-84

US-10-389-417-84

US-10-389-417-84

US-10-389-417-84

US-10-389-417-84

US-10-389-417-84
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Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Maximum DB
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-10-449-379-48	-10-688-01	-10-160-506-6	-10-160-506-6	-10-449-379-6	-10-449-379-	-10-688-015-6	-10-688-015-6	-10-160-506-6	-10-449-379-	-10-688-015-6	-10-160-506-6	-10-449-379-6	-1.0-688-015-6	-10-160-506-5	-10-160-506-6	-10-160-506-6	-10-449-379-5	-10-449-379-6	-10-449-379-6	-10-688-015-5	-10-688-015-6	-10-688-015	-10-160-506-6	-10-449-379-6	-10-688-015-6	-10-160-506-5	-10-449-379-5	688-015-5	-09-874-14
16	16	14	14	16	16	16	16	14	16	16	14	16	16	14	14	14	16	16	16	16	16	16	14	16	16	14	16	16	10
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RESULT:

US-929-66-16

Sequence 16, Application US/09929665

Publication No. US7003001101A1

Sequence 16, Application US/09929665

Publication No. US7003001101A1

APPLICANTE Bander. Neil H.

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION WINBER: US/09/929, 665

CURRENT APPLICATION NUMBER: US/09/929, 665

PRIOR PLING DATE: 1999-07-20

PRIOR PLING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: US 08/838, 682

PRIOR APPLICATION NUMBER: US 08/038, 682

PRIOR APPLICATION NUMBER: US 60/016, 976

PRIOR APPLICATION NUMBER: US 60/016, 976

PRIOR APPLICATION NUMBER: US 60/022, 125

PRIOR APPLICATION NUMBER: US 60/016, 976

PRIOR
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NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                         RESULT 4
US-09-929-546-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Sequence 11, Application US/09929665

Publication No. US2003003101A1

GENERAL INFORMATION:

APPLICANT: Bander, Neil H.

TITLE OF INVENTION: TREATHENT AND DIAGNOSIS OF PROSTATE CANCER

FILE REPERENCE: Lois M. Kwasigroch: BZL 242/024

CURRENT FILING DATE: 2001-08-13

CURRENT FILING DATE: 2001-08-13

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-06-06

PRIOR FILING DATE: 1996-07-16

PRIOR FILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 11

SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 562; DB 10; Length 121; 100.0%; Pred. No. 1.9e-48; ive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                              TITLE OF INVENTION: Neil H.

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
FILE REPERBNCE: Lois M. Kwasignoch: BZL 42/028
CURRENT APPLICATION NUMBER: US/09/929,546
CURRENT PILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/357,708
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ 1D NOS: 21
SOFTWARE: PATCHTIN VERSION 3.0
US-09-929-546-16; Sequence 16, Application US/09929546; Publication No. US20030031673A1; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mus sp.
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CRGANISM: Mus sp.
US-09-929-665-11
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APPLICANT: Rodriguez, Moses
APPLICANT: Rodriguez, Moses
APPLICANT: Miler, David J.
APPLICANT: Miler, David J.
APPLICANT: Miler, David J.
APPLICANT: Pease, Larry K.
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
TITLE OF INVENTION: System
FILE REPERBENCE: 1199-1-005CIP2
CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1996-08-08
PRIOR PRIOR DATE: 1996-08-08
PRIOR PRIOR DATE: 1994-04-29
PRIOR FILING DATE: 1994-04-29
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                                                                           67 RFTGSGSATDFTLTISSVQAEDLADYHCGOGYSYPYTFGGGTKLEIK 113
61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09929546
Fublication No. US20030031673A1
GENERAL INFORMATION:
APPLICANT: BANGET, Nell H.
ITILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
CURRENT FILING DATE: 2001-08-13
FRIOR APPLICATION NUMBER: 08/357,708
FRIOR PRIOR DATE: 1999-07-20
FRIOR PILING DATE: 1999-07-20
FRIOR FILING DATE: 1999-07-20
FRIOR FILING DATE: 1996-05-06
FRIOR FILING DATE: 1996-05-06
FRIOR FILING DATE: 1996-05-06
FRIOR PRIOR FILING DATE: 1996-05-06
FRIOR PILING DATE: 1996-05-06
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100.0%; Score 562; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 107; Conservative 0; Mismatches 0;
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Publication No. US20030185827A1
GENERAL INFORMATION:
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Sequence 34, Application US/08779784

j Publication No. US20020164325A1

j Publication No. US20020164325A1

GENERAL INPORMATION:

APPLICANT: Maller, David J.

APPLICANT: Asakura Kunihiko

TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

TITLE OF INVENTION:

STREET: All Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

CITY: Hackensack

STREET: Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA
                                                                                                                                                                                                                                                   21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                                                                                                                                                                                                              1 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD
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                                                                                                                                                     Gaps
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                                                                                             Query Match 100.0%; Score 562; DB 12; Length 135; Best Local Similarity 100.0%; Pred. No. 2.1e-48; Matches 107; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/10371797
Publication No. US20040001828A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TUSCANO, JOSEPH
APPLICANT: TEDDER, Thomas
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE REFERENCE: 39754-0951
CURRENT APPLICATION NUMBER: US/10/371,797
CURRENT APPLICATION NUMBER: US 60/420,472
PRIOR APPLICATION NUMBER: US 60/420,472
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/359,419
PRIOR APPLICATION NUMBER: US 60/359,419
PRIOR APPLICATION NUMBER: US 60/359,419
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEG ID NOS: 31
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, ORGANISM: homo sapiens
US-10-371-797-31
            ; ORGANISM: Homo sapiens
US-10-372-481-31
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US-10-371-797-31
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LENGTH: 135
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WS-10-066-773-19

WS-10-066-773-19

FUBLICATION NO. US20020132983A1

GENURAL INFORMATION:

APPLICANT: Unuphans, Richard P.

TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antiports PPLICANT: UNUMBER: US/10/006,773

CURRENT PELING DATE: 2001-12-10

PRIOR FILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.1

SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-372-481-31
Sequence 31, Application US/10372481
Sequence 31, Application WS/10372481
Sequence 31, Application WS/10372481
Sequence 31, Application WS/10372481
Sequence 31, Application WS/10372481
SERIER PREPRENCE: Fixeder, Thomas F.
TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 5405.306
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR PAPLICATION NUMBER: US 60/420,472
PRIOR PAPLICATION NUMBER: US 60/420,472
PRIOR APPLICATION NUMBER: US 60/359,419
PRIOR APPLICATION NUMBER: US 60/359,419
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 31
LENGTH: 135
TYPE: PRI
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                                                                                                                                                                              Query Match 100.0%; Score 562; DB 14; Length Best Local Similarity 100.0%; Pred. No. 2e-48; Matches 107; Conservative 0; Mismatches 0; Indels
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; SEQ ID NO 70
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Mus sp. US-10-006-773-19
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Gaps

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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Tarurahita, Nacya
APPLICANT: Tarurahita, Nacya
APPLICANT: Protein Design Labs, Inc.
APPLICANT: NUMBER: US/09/992,524
CURRENT APPLICATION NUMBER: US/09/992,524
CURRENT APPLICATION NUMBER: 09/450,520
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
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Publication No. US20040049014A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
Co, Man Sungliam P.
Landolfi, Nicholas F.
Coelingh, Kathleen L.
Selick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
                                                                                                                                                                                                                                                                                Indels
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100.0%; Pred. No. 9.6e-46;
iive 0; Mismatches 0;
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Pred. No. 2.5e-44;
5; Mismatches 4;
  PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09992524 Patent No. US20020091240A1 GENERAL INFORMATION:
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1 Similarity 91.6%;
98; Conservative 9
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Matches 101; Conservative
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, OTHER INFORMATION: AF2 VL
US-09-992-524-2
                                                                      ; SEQ ID NO 21

: LENGTH: 101

: TYPE: PRT

; ORGANISM: Mus musculus

US-10-010-729-21
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ORGANISM: Mus sp.
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US-10-389-417-84
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US-10-010-729-21

Sequence 21, Application US/10010729

Publication No. US20030185827A1

GENERAL INFORMATION:

APPLICANT: Rodisquez, Moses

APPLICANT: Rodisquez, Moses

APPLICANT: Miller, David J.

TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and

TITLE OF INVENTION: System

TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous

TITLE OF INVENTION: System

TITLE OF INVENTION: System

TITLE OF INVENTION: System

FILE REFERENCE: 1199-1-005CIP2

CURRENT PILING DATE: 2000-12-05

PRIOR APPLICATION NUMBER: 09/730, 473

PRIOR APPLICATION NUMBER: 09/322, 862

PRIOR APPLICATION NUMBER: 09/322, 862

PRIOR PILING DATE: 1999-05-30

PRIOR FILING DATE: 1999-05-30

PRIOR PILING DATE: 1999-05-30

PRIOR APPLICATION NUMBER: 09/322, 862

PRIOR APPLICATION NUMBER: 09/322, 863

PRIOR PILING DATE: 1999-06-08

PRIOR APPLICATION NUMBER: 09/322, 863

PRIOR PILING DATE: 1996-09-08

PRIOR PILING DATE: 1996-09-08

PRIOR PILING DATE: 1996-09-08

PRIOR PILING DATE: 1996-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.6%; Score 554; DB 8; Length 128; 99.1%; Pred. No. 1.3e-47; ive 0; Mismatches 1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
FILING DATE: 07-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1199-1-001 CIPA
                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION UNMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REPERENCE/DOCKET NUMBER: 1199 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.1;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201-343-1684
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30 NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVHD 89
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APPLICATION NUMBER: US/10/389,155 FILING DATE: 13.Mar-2003
PRIOR APPLICATION DATA:
APPLICATION ANTH:
APPLICATION NUMBER: US/99/325,000
FILING DATE: 01.JUN-1999
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-DE-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 128-EB-1989
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-DE-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 2.1e-43;
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                      PRICE APPLICATION NUMBER: 09/718, 993
PRICE FILING DATE: 2000-11-22
PRICE FILING DATE: 2000-11-22
PRICE FILING DATE: 1995-06-07
PRICE FILING DATE: 1995-06-07
PRICE FILING DATE: 1990-12-19
PRICE APPLICATION NUMBER: 07/590,275
PRICE APPLICATION NUMBER: 07/590,275
PRICE APPLICATION NUMBER: 07/590,275
PRICE APPLICATION NUMBER: 07/290,975
PRICE FILING DATE: 1999-02-13
PRICE FILING DATE: 1999-02-13
PRICE FILING DATE: 1998-12-28
NUMBER: 07/290,975
NUMBER: 07/290,975
SEQ ID NOS: 113
SEQ ID NOS: 113
       2003-05-30
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l Similarity 90.7%;
97; Conservative
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       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-389-155-84
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Best Local S:
Matches 97
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Publication No. US20040058414A1
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
APPLICANT: Co. Man Sung
APPLICANT: Co. Man Sung
APPLICANT: Schneider, William
APPLICANT: Arbider, Nicholas
APPLICANT: Selick, Harold
ITLE OF INVENTION: Improved Humanized Immunoglobulins
FILE REPERENCE: 05882.0078.CNUS01
CURRENT APPLICATION NUMBER: US/10/452,357
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                             STREET: Two Embarcadero Center, Bighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
91.1%; Score 512; DB 12;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 97; Conservative 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-M2-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-UN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-PEB-1969
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-DEC-1980
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-UNN-1995
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 136 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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9

Gaps

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Sequence 48, Application US/10160506

Publication No. US20030161832A1

GENERAL INFORMATION

APPLICAT: Bander,

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING

TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR

TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR

TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR

TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN

FILE REFERENCE: 10448-16201

CURRENT APPLICATION NUMBER: 60/324,100

PRIOR APPLICATION NUMBER: 60/324,100

PRIOR FILING DATE: 2002-03-08

NUMBER OF SEQ ID NOS: 128

SOFTWARE: FAST SEQ ID NOS: 128

SOFTWARE: FAST SEQ ID NOS: 128

SEQ ID NO 48

LENGTH: 107

TYPE: PRI

TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFTGSGSATDFILTISSVQTEDLVDYYCGQSYTFPYTFGGGTKLEMK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.1%; Score 512; DB 15; Length 136; Best Local Similarity 90.7%; Pred. No. 2.1e-43; Matches 97; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 136 amino acids
| TYPE: amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| MOLECULE TYPE: protein
| SEQUENCE DESCRIPTION: SEQ ID NO: 84:
| US-10-389-155-84
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US-10-160-506-48
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 16, 2004, 11:08:06; Search time 11.5157 Seconds (without alignments) 893.780 Million cell updates/sec protein search, using sw model OM protein Run on:

US-09-889-300A-2 562 1 NIVMTQSPKSMSWGVGERVT......CGQGYSYPYTFGGGTKLEIK 107 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	g kappa chain pr	g kappa cha	g kappa chain V	g kappa chain pr	g light chain V	g kappa chain V	g light chain V	g light chain V	nti-DNA autoanti	g kappa chain V	g kappa chain V	g kappa chain V	g kappa chain pr	g kappa chain pr	g kappa chain V	g kappa chain V	kappa cha	g kappa chain pr	g kappa chain v	nti-idiotypic an	g kappa chain V	g kappa chain V	g light chain V-	g kappa chain V	g kappa chain -	g lambda cha	g kappa chain V	g kappa chai	g kappa chain V
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kappa chain V	PL7-6 antibody 119 Ig light chain V r	kappa chain V	kappa chain V	kappa chain	kappa chain V	kappa chain	kappa chain '	kappa	kappa chain -	kappa	kappa chain V-	kappa chain	kappa	light chain '
B28195	~ ~	H38601	PL0263	PC1214	PL0083	S52793	PT0356	B49047	S40317	S31981	K4HULN		S41393	PT0407
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107	113	100	113	134	108	129	118	108	129	109	114	111	112	113
	40.1	σ	Ø	σ	σ	o	о О	68.8	Θ.	œ	œ,	æ.	68.1	œ.
394	თთ		σ	391	389.5	œ		387	α	α	384	œ	382.5	82.
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 KWMS21 19 Kappa chain precursor V region (MOPC 21) - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1980 #sequence revision 02-Apr-1982 #text_change 22-Jun-1999 C;Date: 31-Mar-1980 #sequence revision 02-Apr-1982 #text_change 22-Jun-1999 C;Date: 31-Mar-1980 #sequence revision 02-Apr-1982 #text_change 22-Jun-1999 C;Date: 31-Mar-1980 #sequence of an immunoglobulin mRNA using specific priming and the did A;Reference number: A93736; MUID:82059477; PMID:6170937 A;Accession: A93736 A;Accession: A93736 A;Residues: nRNA A;Residues: 1-136 < HAM> R;Svasti, J.; Milstein, C.	Blochem. J. 128, 427-441, 1972. AjTitle: The complete amino acid sequence of a mouse kappa light chain. AjReference number: A90262, MUID:73053310; PMID:4638343 AjContents: myeloma protein MOPC 21 AjAccession: A90262 AjMolecule type: protein AjResidues: 30-136 <sva> Ribin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.F. J. Biol. Chem. 269, 2805-2813, 1994 AjTitle: Topology of an amiloride-binding protein. AjReference number: A49982; MUID:94132051; PMID:8300613</sva>	A, Accession: B49882 A, Accession: B49882 A, Status: preliminary; not compared with conceptual translation A, Molecule type: mRNA A, Residues: 30-136 < LIN> A, Cross-references: GB-124803; NID: 9452098; PIDN: AAC37684.1; PID: 9452099 A, Experimental source: clone BA7.1 C, Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka,
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hain disultide bonds. In some cases, such as IgA and IgM, the subunits associate into 1-6, Superfamily: immunoglobulin V region, immunoglobulin homology
C; Superfamily: immunoglobulin V region, immunoglobulin homology
C; Keywords: heterotetramer, immunoglobulin
F;1-29/Domain: signal sequence #status predicted <SIG>F;0-10-5/Product: Ig kappa chain V region (MOPC 21) #status experimental <MAT>F;0-10-5/Product: Immunoglobulin homology <IMM>F;115-110/Domain: immunoglobulin homology <IMM>F;125-117/Disulfide bonds: #status predicted

ö Gaps .. 0 Length 136; 0; Indels Query Match
100.0%; Score 562; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 107; Conservative 0; Mismatches 0;

1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60 30 NIVMTQSPKSMSMSVGERVTLTCKASENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVPD 89 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107 ò g à

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A,Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated gern A,Reference number: A33932, MUID:892823; PMID:2499887
A,Reseasion: 133932
A,Status: preliminary; not compared with conceptual translation
A,Molecule type: mRNA
A,Residues: 1-118 < BAC>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;39-113/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ignation of the second section (anti-DNA, DP9VK and DP17VK) - mouse (fragment)

C;Species: Mus musculus (bouse mouse):
C;Species: Mus musculus (bouse mouse):
C;Accession: PL0268

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
B;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
A;Thitle: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Recession: PL0268
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroterramer; immunoglobulin
E;1-22/Region: framework I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig light chain V region - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: S38713
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A.Reference number: S38713
A.Accession: S38713
A.Accession: S38713
A.Accession: S38713
A.Accession: S38713
A.Accession: S38713
A.Accession: MRNA
A.Reference number: S18713
A.Accession: S38713
C.Accession: S38713
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A.Accession: S38713
A.Accession: S38713
C.M.C. CIM.
A.Residues: I-107
C.M.C. CIM.
A.Residues: I-107
C.M.C. CIM.
A.C. CIM.

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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 118;
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88.8%; Pred. No. 9.8e-37;
tive 6; Mismatches 6; Indels
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Best Local Similarity 100.0%; Pred. No. 4.8e-37;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYP 118
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Best Local Similarity 88.8%
Matches 95; Conservative
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533122
Ig Abachain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change: M.; Rifaldi, B.; Marc Submitted to the EMBL Data Library, May 1993
A;Reference number: S33131
A;Reference number: S33131
A;Recession: S33132
A;Reterence number: Manary
A;Molecule type: DNA
A;Residues: 1-107 <-TEM>A;Residues: 1-107 <-TEM>A;Residues: 1-107 <-TEM>C;Reywords: heterotetramer; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <-INMA>
                                                                                                                                                                                                                                                                                                                                                                                                                           anti
                                                                                                                                                                                                                                                                                                                                                                                                                           and antibody properties of
                                                                                                                                                                 Ig Kappa chain V region (129) - mouse C.Species: Mus musculus (house mouse) C.Species: Mason, S.; Campos Gonzalez, R.; Glenney Jr., J.R.
C.A. Chem. 266, 6607-6613, 1991
A.Title: Heavy and light chain variable region sequences and antibody properties A.Title: Heavy and light chain variable region sequences and antibody properties A.Totle: Heavy and light chain variable region sequences and antibody properties A.Totle: Heavy and light chain variable region sequences and antibody properties A.Totle: Heavy and light chain variable region sequences and antibody properties A.Totle: Heavy and light chain variable region sequences and antibody properties A.Totle: Heavy and Light compared with conceptual translation A.Molecule: type: mRNA
A.Molecule: T.II - RUFA;
C.Superfamily: immunoglobulin V region; immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin P:19-93/Domain: immunoglobulin homology < IMM>
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133932
133932
19 kappa chain precursor V region (E7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: 133932
Brocala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
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Pred. No. 1.4e-38;
3; Mismatches 5; Indels
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ses 99; Conservative
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Best Local Similarity
Matches 105; Conserva
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us-09-889-300a-2.rpr

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anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0204
R;Smith, R, G:, Voss Jr., E.W.
R) Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from h A;Reference number: PL0198; MuID:90309768; PMID:2114528
A;Accession: PL0204
A;Residues: 1-108 cSMI>
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                                                         1 SPKSMSMSVGERVTLSCKASENVGTYVSWYQQKP-QSPQLLIYGASNRYTGVPDRFTGSG 59
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C;Species: Mus musculus (house mouse)
C;Accession: S3192
R;Izui, S.
B;Izui, S.
B;Neference number: S32185
A;Reference number: S32185
A;Refer
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <INM>
    7 SPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSG
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                                                                                                                                                                                                                                                 60 SATDFTLTISSVQAEDLADYHCGQSYSYPFTF 91
                                                                                                                                                                      67 SATDFTLTISSVQAEDLADYHCGQGYSYPYTF
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Best Local Similarity
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Ig light chain V region (clone 17s.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1070
C;Accession: PH1070
D.M.; VT.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B C;Accession: PH1070
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1070
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-96 <TIL)
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superimental; immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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Iglight chain V region (clone 165.3m) - mouse (fragment)

Species was musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PHIOTI

B. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B G

A;Reference number: PHO971; MUID:92381444; PMID:1512540

A;Status: nucleic acid sequence not shown

A;Status: nucleic acid sequence not shown

A;Reaidues: 1-91 < TIL.

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                  Length 107;
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80.8%; Score 454; DB 2; Length 96;
Best Local Similarity 93.9%; Pred. No. 2.9e-33;
Matches 92; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                          Score 459; DB 2; Length 10 Pred. No. 1.2e-33; 7; Mismatches 12; Indels
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F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4
                                                                                                                                                                                                              81.7%;
82.2%;
                                                                                                                                                                                                              Query Match
Best Local Similarity 82.2
Matches 88; Conservative
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Best Local Si
Matches 86;
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61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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$32191
Ig kappa chain V region - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: $32191
R;Zui, S.
submitted to the EMBL Data Library, February 1993
A;Recerance number: $32185
A;Accession: $32191
A;Accession: $32191
A;Accession: $32191
A;Accession: $32191
A;Accession: $32191
C;Coss_references: EMBL:X70095; NID:9288260; PIDN:CAA49700.1; PID:9288261
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                                   .Species: Mus musculus (house mouse)
Species: Mus musculus (house mouse)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                   CiSpecies: Mus musculus (house)
CiSpecies: Mus musculus (house)
CiDate: O6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
CiDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
CiDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
CiDate: 06-Jan-1995 #sequence_revision 06-Jan-1994
Rishipatov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
A;Reference number: 842466
A;Accession: 842466
A;Accession: 842466
A;Accession: Preliminary
A;Accession: Preliminary
A;Accession: Preliminary
A;Accession: Intro CAHL
A;Accidence: EMBL: X78108; NID: 9460824; PIDN: CAA54998.1; PID: 9460825
C;Superfamily: immunoglobulin Wregion; immunoglobulin homology
C;Keywords: heterotectamer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <INM>
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Llarity 78.5%; Pred. No. 5.5e-31;
Conservative 10; Mismatches 13; Indels
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Ig kappa chain V region - mouse
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Matches 84; Conserv
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KVMS11
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A, Molecule type: protein
A, Residues: 30-149 < SMI>
A, Residues: 30-149 < SMI>
A, Residues: 30-149 < SMI>
A, Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not 5, Comment: The mature chain has 12 additional residues at its amino end, due to a tant 42 corresponds to the amino-terminal residue of typical kappa chains.
C, Complex: An immunoglobulin heteroterramer subunit consists of two identical light () hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C, Keywords: duplication; heterotetramer; immunoglobulin homology
C, Keywords: duplication; heterotetramer; immunoglobulin pomology
F;30-149/Product: Ig kappa chain V region (MPOII) #status experimental < MAT>
F;57-131/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S04577
R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.
Submitted to the EMBL Data Library, March 1989
A;Description: Complexity, polymorphism and connectivity of murine V(kappa) gene fami: A;Reference number: S04577
A;Accession: S04577
                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 41-149 «RAB»
R,Smith, G.P.
Biochem. J. 171, 337-347, 1978
A,Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC
A,Reference number: A90298; MUID:78186617; PMID:418775
A;Accession: A90823
A;Molecule type: DNA
A;Residues: 1-71 - KEL>
A;Rolecule type: DNA
A;Residues: 1-71 - KEL>
A;Note: the sequence was determined from the differentiated gene
R;Rabbitts, T.H.; Hamlyn, P.H.; Matthyssens, G.; Roe, B.A.
Can. J. Blochem. S8, 176-187, 1890
A;Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
A;Reference number: A90753; MUID:80176554; PMID:6245773
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.1%; Score 422; DB 1; Length 149; Best Local Similarity 78.5%; Pred. No. 2.9e-30; Matches 84; Conservative 8; Mismatches 15; Indels
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Matches 81; Conserv
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A; Residues: 1-127 < KOF>
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FQUADEA

FQUADEA

FQUADEA

C, Species: Mus musculus (house mouse)

C, Species: Mus musculus (house mouse)

C, Species: Mus musculus (house mouse)

C, Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C, Accession: PQ0265

R, Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.

R, Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.

R, Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal

A, Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal

A, Reference number: P00265; MUID:92039046; PMID:1937027

A, Accession: P00265

A, Molecule type: mRNA

A, Residues: 1-119 *LOH;

A, Accession: P00265

A, Multiple in recognizes a restricted idiotype associated with antibodies spec

C, Comment: This protein recognizes a restricted idiotype associated with antibodies spec

C, Superfamily: immunoglobulin N vegion; immunoglobulin

C, Keywords: heterotetramer; immunoglobulin

F, 28-102/Domain: immunoglobulin homology and MN>

F, 26-46/Region: complementarity-determining 2

F, 56-68/Region: complementarity-determining 3

F, 101-109/Region: complementarity-determining 3
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81 RFTGSGSGTDFTFTISSVQVEDLAVYFCQQHYSSPWTFGGGGTKLEIK 127
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Search completed: August 16, 2004, 11:09:11 Job time : 11.5157 secs

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MEDLINE=82059477; PubMed=6170937;
Hamlyn P.H., Gait M.J., Milstein C.;
Homplete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing.";
Nucleic Acids Res. 9:4485-4494(1981).
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 30-136.
MEDLINE=73053310; PubMed=4638343;
Svasti J., Milstein C.;
"The complete amino acid sequence of a mouse kappa light chain.";
Biochem. J. 128:427-444(1972).
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PPO1159
PPO116660
PPO116666
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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PIR; A93736; KYMS21.
PDB; 1IGC; 03-UUN-95.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR0077110; Ig-1ike.
InterPro; IPR003596; Ig-v.
Pfam; PF0047; ig: 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
SIGNAL 30 136 IG ARPPA CHAIN V-V R
CHAIN 30 136 IG CHAIN V-V R
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig kappa chain V-V region MOPC 21 precursor.
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KV2G MOUSE
KV2G HUMAN
KV1G HUMAN
KV1C HUMAN
KV1C HUMAN
KV3M MOUSE
KV3M MOUSE
KV3A MOUSE
KV3A MOUSE
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 RESULT 1
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725.728 Million cell updates/sec
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562
1 NIVWTQSPKSMSWGERVT......CGQGYSYPYTFGGGTKLEIK 107
                                                                                            August 16, 2004, 11:08:06; Search time 7.67713 Seconds
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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                                                                                                                                                                                                                                                    141681 segs, 52070155 residues
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KV1R_HUMAN
KV3H_HUMAN
                                                                 - protein search, using sw model
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Maximum DB
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P01632;
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                                                                                                     30 NIVMTQSPKSMSMSVGERVTLTCKASENVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
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Biochem. J. 171:337-347(1978).

Biochem. J. 171:337-347(1978).

-!- MISCELLANDOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL RESIDUE OF TYPICAL KAPPA CHAINS.
                                                                  1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD
                            Gaps
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BEDLINES 20175554; PubMed-6245773;
Rabbitts T.H. Hamlyn P.H., Matthyssens G., Roe B.A.;
"The variability, arrangement, and rearrangement of immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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MEDLINE-83001944; PubMed-6288267;
Kelley D.B., Coleclough C., Perry R.P.;
"Functional significance and evolutionary development of the S.-terminal regions of immunoglobulin variable-region genes.";
Cell 29:681-689(1982).
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FRAMEWORK-1.
CROMPLEMENTARITY-DETERMINING-1.
COMPLEMENTARITY-DETERMINING-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                           90 RFTGSGSAIDFILIISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 136
                                                                                                                                                   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
7e-53;
hadels 0; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                  149 AA
                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V-V region MPC11 precursor.
Mus musculus (Mouse).
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
        100.08;
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        1 Similarity 100.
107; Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
"Nucleic acid and protein sequences of phosphocholine-binding light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                102 RFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 148
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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                                                                                                                                                                                             Length 149;
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                              15; Indels
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                                                                                                                                              16434 MW; B0480C87B682AC3E CRC64;
                                                                                                                                                                                             Score 422; DB 1;
Pred. No. 6.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region S107A.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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InterPro; IPR003596; Ig_v.
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78.5%;
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PIR; A01915; KVMS7A.
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NCBI_TaxID=9606
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                                NIVMTOSPKSMSMSVGERVTLICKASENV-----VTYVSWYQQKPEQSPKLLIYGASNR 54
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                                                                                                                                              Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"The primary structure of a monoclonic immunoglobulin-L-chain subgroup IV of the kappa type (Bence-Jones protein Len).";
Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
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Pfam; PF00047; ig; 1.

SMAT; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Bence-Jones protein; 3D-structure.

I 23 COMPLEMBNTARITY-DETERMINING-1.

COMPLEMBNTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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65.5%; Pred. No. 6.4e-34;
tive 18; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                             21-UUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11g kappa chain V-IV region Len.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                              114 AA.
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BY SIMILARITY.
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PDB; IEEQ; 03-FEB-01.
PDB; IEK3; 06-MAR-01.
PDB; ILVE; 21-JAN-98.
PDB; 31VE; 18-MAY-99.
PDB; 51VE; 18-MAY-19.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005955; F:antigen binding; NAS.
INCERPO; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE=76004342; PubMed=50995;
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                                                                                                                                                                                                                                                                                                              STANDARD;
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Best Local Similarity
Matches 74; Conserv
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                                                                                                                                                                                                                                                                                                           KV4A HUMAN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marsh P.;
Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14966 MW; 6413A22FD0738832 CRC64;
                                           01-JAN-1988 (Rel. 06, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-IV region B17 precursor.
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134 AA
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 13:6531-6544(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PFC0047; ig; 1. 3—. SMART, SMC0406; IGV; 1. PROSITE; PSC0835; IG LIKE; 1. Immuncglobulin V region; Signal. SIGNAL
                                                                                                                                                               Eukaryota, Metazoa, Chordata;
Mammalia, Eutheria, Primates;
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1114
121
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114
                                                                                                                   Ig kappa chain V-IV r
Homo sapiens (Human).
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KVIO HUMAN STANDARD; I C PO1607; DT 21-JUL-1986 (Rel. 01, Created)
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68; Conservative
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34
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107
107
31
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Best Local Si
Matches 68,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                        Scand. J. Immunol. 5:677-684 (1976).
-!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                         Capra J.D., Klapper D.G.;
Complete amino acid sequence of the variable domains of two human
IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
specificities...;
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 375; DB 1; Length 108; 65.4%; Pred. No. 4.3e-33;
                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                       19; Indels
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      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
19 kappa chain V-I region Lay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
11g kappa chain V-1 region WAT.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches
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HSSP; PO1607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005575; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR07110; Ig-like.
InterPro; IPR03596; Ig_V.
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                                                                                                MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                            PEGM; PEGOGAT; 19; 1.
SMART; SMO0406; 1GV; 1.
PROSTIE; PSS0835; 1G LIKE; 1.
Immunoglobulin V region.
POMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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88
108
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tes 70; Conserv
                                                                      NCBI_TaxID=9606;
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P80362;
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SEQUENCE
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                                                                                                                                                                                                              Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Pepp R.A., Solomon A.;
"Characterization and preliminary crystallographic data on the Virelated fragment of the human KI Bence Jones protein Wat.";
J. Mol. Biol. 147.185-193(1981).
J. Mol. Biol. 147.185-193(1981).
PDB; JWTL, 01-NOV-94.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000523; F:antigen binding; NAS.
GO; GO:000582; P:immune response; NAS.
InterPro; IPR007110; IG-1ike.
Solomon A., Stevens F.J., Schiffer M.; "Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; i. SMART; SM00406; IGV; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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63.6%; Pred. No. 1.5e-32;
ive 20; Mismatches 19;
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TN -> SD (IN REF.
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                                                                                                                   Biochemistry 33:14848-14857(1994)
                                                                                                                                                               SEQUENCE OF 1-35.
MEDLINE=81267384; PubMed=6167731;
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DOMAIN
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                                                                                                                 Palm W., Hilschmann N., "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their
                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=76039568; PubMed=1162131;
Epp O. Lattman E.E. Schiffer M., Huber R., Palm W.;
The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein RBI refined at 2.0-A resolution.";
elochemistry 14:4943-4925(1975).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; i. 7—8ART; 8000407; ig; i. PROSITE; PS50835; IG LIKE; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Bence-Jones protein; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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11902 MW; 9E8143E1188BCE2A CRC64;
                                                                                                                                                                                        combining site.";
Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975)
                                                                                                                                                                                                                                                                                                                        !- MISCELLANEOUS: This is a Bence-Jones protein.
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig kappa chain V-I region Rei.
                                                                                                                                                                                                                                                                                                                                  PIR; A91663; KIHURE.
PDB; 1REI; 17-FEB-84.
PDB; 1ARZ; 12-NOV-97.
PDB; 1BWW; 29-DEC-99.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005923; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00110; Ig-1ke.
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                                                                                                         MEDLINE=76023758; PubMed=809329;
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449
55
88
97
107
88
                                     Homo sapiens (Human)
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108 AA;
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Length 108;

Score 365; DB 1; Pred. No. 5e-32;

64.9%; 63.2%;

Query Match Best Local Similarity

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                                                       1 DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS
                                   1 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYTGVPD
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.6%; Score 363; DB 1; Length 108;
llarity 63.6%; Pred. No. 8.1e-32;
Conservative 17; Mismatches 22; Indels
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
20; Indels
                                                                                                                                 RFSGSGSGTDYTFTISSLOPEDIATYYCQQYQSLPYTFGQGTKLQI
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01-07N-1988 (Rel. 06, Last sequence update)
15-01L-1999 (Rel. 38, Last annotation update)
11g kappa chain V-IV region JI precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
119 kappa chain V-I region BAN.
Homo sapiens (Human).
                                                                                                                                                                                                                                          108 AA
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"Polymorphism in a kappa I primary (AL) amy
M.D. Immunol. 13.73-78(1986).
PIR, AOL878; KIHUBN.
HSSP; PROB362; JMT.
GSP; PROB362; JMT.
GSP; PROB362; JMT.
GSP; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005578; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-like.
 19; Mismatches
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Amyloid.
DOMAIN
 67; Conservative
                                                                                                                                                                                                                                          STANDARD;
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35
50
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108 AA;
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Best Local Similarity
Matches 68; Conserv
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KV4B HUMAN
ID KV4B HUMAN
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SEQUENCE
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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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MEDLINE=79012520; PubMed=99744;
MECKGAR D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
                                                                                                                         HODDE-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                         Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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-!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
HSSP, PO1679; 2FBJ.
InterPro; IPRO07110; Ig-like.
InterPro; IPR003556; Ig-v.
Pfam; PP00047; ig; 1.
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 FRAMEWORK-1,
34 COMPLEMENTARITY-DETERMINING-
56 COMPLEMENTARITY-DETERMINING-
56 FRAMEWORK-2,
97 COMPLEMENTARITY-DETERMINING-
107 FRAMEWORK-3,
107 FRAMEWORK-4,
88 BY SIMILARITY.
108 BY SIMILARITY.
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Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-III region ABPC 22/PC 9245.
Mus musculus (Mouse).
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HSSP, P80362; UWTL.
GO, GO:0003823; F:antigen binding; NAS.
GO, GO:0003823; F:antigen binding; NAS.
GO, GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PR00047; ig; 1.
PR0SITE; P850835; IG, ILKE; 1.
PROSITE; P850835; IG, ILKE; 1.
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                                                                                                              subgroups.";
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P01662;
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NON TER
SEQUENCE
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KV3J MOUSE
                               STATE TELEVISION NO CONTRACT TO CONTRACT TO CONTRACT TELEVISION NO C
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                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                   Zachau H.G.; "Subgroup IV of human immunoglobulin K light chains is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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63.7%; Pred. No. 1.2e-31;
ive 19; Mismatches 15
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Hau.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 13:6515-6529(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART, SM00406, ĬĠv, 1.
PROSITE, PS50835, IG LIKE, 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z00022; CAA77317.1; -. PIR; A01904; K4HUJI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuery Match
Best Local Similarity 63...,
Conservative
72; Conservative
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133 AA;
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FRAMEWORK-3
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59.8%; Fr.
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Best Local Similarity 61.73
Matches 66; Conservative
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35
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89
23
108
AA;
79
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120
45
129 AA;
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les 64; Conserv
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                                                                                                                                                                                                                                                                                                                         1 NIVMIQSPKSMSMSVGERVILICKASENVVIY----VSWYQQKPEQSPKLLIYGASNRYI
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-85014148; PubMed=6091049;
Michock H.G., Combriato G., Zachau H.G.;
Mimunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCPI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                              57 GVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINIG-1.
                                                                                                                                                                                                                                               63.9%; Score 359; DB 1; Length 111;
63.1%; Pred. No. 2.2e-31;
iive 17; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                      FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                       COMPLEMENTARITY-DETERMINING-1
                                                                                                                                     COMPLEMENTARITY-DETERMINING-3 FRAMEWORK-4.
                                                                                                                                                                                                               12041 MW; D7DF0609303453CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Daudi precursor.
                                                                                                                                                                             SIMILARITY.
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GO, GO:0005576, C:extracellular; NAS.
GO, GO:0005823, F:antigen binding; NAS.
GO, GO:0006955, P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SWART; SW00406, IGv; 1.
PR003TB; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                        FRAMEWORK-1
                                                                                                                            FRAMEWORK-3
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                     Conservative
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56
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339
54
61
103
111
111 AA;
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Best Local Similarity
Matches 70; Conserv
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KV1X_HUMAN
ID _KV1X_HUMAN
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                                                                                                                                                                                                                                                                                                                                         23 DIQMIQSPSSLSASVGDRVIITCRAGHNIINFLSWYQQKPGRAPILLIYAVSNLQVGVPS 82
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Bulitz M., Kley H.-P., Zeitler H.-J.;

Bulitz M., Kley H.-P., Zeitler H.-J.;

Entity M. Kley H.-P., Zeitler H.-Bence-Jones protein Kue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";

Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).

-! MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-! MISCELLANEOUS: This is a Bence-Jones protein.
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21-UUL-1996 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Kue.
17 kappa chain V-I region Kue.
18 kappa chain W-I region Kue.
19 kappa chain W-I region Kue.
19 kappa chain W-I region Kue.
19 kappa chain W-I region Kue.
10 kappa chain W-I region Kue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                            63.9%; Score 359; DB 1; Length 129; 59.8%; Pred. No. 2.7e-31; ive 19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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56 COMPLEMENTARITY-DETERMINING-
88 COMPLEMENTARITY-DETERMINING-
107 FRAMEWORK-4.
88 BY SIMILARITY.
108
108
112127 MW; 906679A5D90E4E98 CRC64;
                                                                                                                         14235 MW; CAF076BC7E5574C8 CRC64;
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                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, A01870, KLHUKU.
HSSP, P01607, IREI.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
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61 RFSGSGSGTEFTLTINSLQPDDFATYYCQQYSRYPYTFGQGTKLDIK 107

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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTY----VSWYQQKPEQSPKLLIYGASNRYT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                  Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                        SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;
Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.7%; Score 358; DB 1; Length 111; Best Local Similarity 61.3%; Pred. No. 2.9e-31; Matches 68; Conservative 21; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12099 MW; EC46C9D259213BE4 CRC64;
                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 3741/TEPC 111.
                       111 AA.
                                                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK-1
                       PRT;
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                               Nature 276:785-790(1978).
                      STANDARD;
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                    KV3H MOUSE
P01660;
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RESULT 15
KV3H_MOUSE
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57 GVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTXLEIK 107 ò d

g

Search completed: August 16, 2004, 11:08:35 Job time : 7.67713 secs

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August 16, 2004, 11:08:06; Search time 31.6682 Seconds (without alignments) 1066.069 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sp bacteria: *
sp_tungi: *
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sp_invertebrate: *
sp_mammal: *
sp_mc: *
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Maximum DB seq length: 2000000000
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sp_rodent:*
sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ulusamamajo musculu	Q9jl74 mus musculu	Q96sa9 homo sapien	Q9ul77 homo sapien	Q9ul78 homo sapien	Q9erz9 mus musculu		Q99m37 mus musculu	Q7z473 homo sapien	Q9ul79 homo sapien	Q7z3y4 homo sapien		Q9ul81 homo sapien	Osvci6 mus musculu	Q8vc55 mus musculu	0.2
SUMMARIES	di	Q8VIJ0	Q9JL74	Q96SA9	Q9UL77	Q9UL78	Q9ERZ9	Q9UL85	Q99M37	Q7Z473	Q9UL79	Q7Z3Y4	Q9UL70	Q9UL81	. Q8VCI6	Q8VC55	Q9UL83
	th DB	08 11	99 11	07 4	08 4	09 4	07 11	09 4	38 11	34 4	08 4	36 4	08 4	07 4	38 11	239 11	08 4
	Query Aatch Length			-													
φė	Query	72.2	67.3	65.6	65.7	65.2	65.1	64	64.7	63.7	63.5	63.5	63.0	62.5	62.4	61.8	61.7
	Score	406	378	370.5	369	366.5	366	363.5	363,5	358	357	357	354	351.5	350.5	347.5	347
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8 1 9 3 3		88	ALIGNMENTS PRT; 108 AA. Created) Last sequence update)
11 Q7TMK3 11 Q8K1F3 11 Q920E9 11 Q8K1F1 11 Q7TS98		0 00 0 00	ALIG PRT; 20, Created 20, Last see
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E E C	`	29 331.5 30 31.5 30 31.5 31.5 31.5 31.5 31.5 31.5 31.5 31.5	RESULT 1 QBVIJO ID QBVIJO AC QBVIJO; DT 01-WAR-2002 DT 01-WAR-2002

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01 VIJAR-2002 (TrEMBLrel. 20, Last sequence update)

01 -NAR-2003 (TrEMBLrel. 25, Last annotation update)

01 -OCT-2003 (TrEMBLrel. 25, Last annotation update)

E Anti-DNA light chain (Fragment).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malkiel S., Liao L., Cunningham M.W., Diamond B.,
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
Infect. Immun. 68:5803-5808 (2000).
BMBL, ARZ06032; AARF09330.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
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                                                                                  61 RFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK 107
                                   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 67.3%; Score 378; DB 11; Length 99; Best Local Similarity 74.7%; Pred. No. 2.5e-33; Matches 74; Conservative 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                         01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;
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                                                                                                                                                                                                                                                                                          99 AA.
                                                                                                                                                                                                                                                                                          PRT;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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1 NIVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPD 60
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                  Match 65.9%; Score 370.5; DB 4; Length 107; Local Similarity 65.4%; Pred. No. 1.8e-32; les 70; Conservative 19; Mismatches 17; Indels 1;
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SEQUENCE FROM N.A.
MUX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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EMBL, AF053037; AAD56273.1; -.
PIR, 849047; B49047.
PIR, 534083; S34083.
HSSP, POLGO7, 1RRI.
InterPro; IRR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 108 AA
Ffam, PF00047; ig, 1. SMART, SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
Choning and sequencing of the light chain fragment of variable region genes of an anti-hTNF-a monoclonal antibody.";
J. Cell. Mol. Immunol. 12:21-26(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MTQSPKSMSWGERVTLTCKASENWV-----TYVSWYQQKPEQSPKLLIYGASNRYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAWYQKKPGQSPELLVYFASTRESG
            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE P. Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.,

"Construction and sequencing of the single-chain antibody gene of human TNP-alpha specific monoclonal antibody.",

Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.1%; Score 366; DB 11; Length 107; Best Local Similarity 64.5%; Pred. No. 5.6e-32; Matches 69; Conservative 17; Mismatches 15; Indels 6
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                                                                                                                                                                                                                                                                               Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF262753, AAG23804.1; -.
R PDB; 2AP2; 24-NOV-99.
R PDB; 43CA; 24-JUL-02.
R InterPro: IPR007110; Ig-11ke.
R InterPro: IPR007110; Ig-11ke.
R InterPro: IPR007110; Ig-11ke.
R SNART; SM00406; IgV; 1.
R SNART; SM00406; IgV; 1.
R SNART; SM00406; IGV; 1.
R NON TER 107 107 107
S SEQÜENCE 107 AA; 11784 MW; 2B15EBA6604A26G3 CRC64;
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10-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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   Mus musculus (Mouse)
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Best Local Similarity 65.4%; Pred. No. 5.1e-32;
Matches 70; Conservative 20; Mismatches 16; Indels 1; Gaps
                                                                                                                                                                  Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSERZ9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti human TNF-alpha light chain variable region (Fragment).
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                             Q9UL78
Q9UL78,
01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                             fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, A30601, A30601.
PIR, A30601, A30601.
PIR, A30601, B30601.
PIR, B30607, B30601.
PIR, B30607, B30601.
PIR, B30607, B30601.
PIR, C30609, C30608.
PIR, C30609, C30608.
PIR, C30609, C30608.
PIR, D30609, D30608.
PIR, D30609, D30608.
PIR, P30609, P30608.
PIR, P30609, P30609.
PIR, P40965, P40965, P40965.
PIR, P40965, P40965.
PIR, P40965, P40965.
PARM, P500047, 19; 1.
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NON TER 109 109
SEQUENCE 109 AN
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                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                 NCBI_TaxID=9606;
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RESULT 5
Q9UL78
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RESULT 8 Q99M37

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Strausberg R.L., Fringold E.A., Grouse L.H., Derge J.G.,
Klausberg R.L., Fringold E.A., Grouse L.H., Derge J.G.,
Klausberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Ronnetein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worlby D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevcherko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
K.Zywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IVMIQSPKSMSMSVGERVILICKASENVVIYVSWYQQKPEQSPKLLIYGASNRYIGVPDR
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Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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63.7%; Score 358; DB 4; Length 234;
Best Local Similarity 61.3%; Pred. No. 1.1e-30;
Matches 65; Conservative 21; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC056256; AAH56256.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                          234 AA
                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
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Q9UL79;
01-MAY-2000 (TEMBLFE1. 13,
01-MAY-2000 (TEMBLFE1. 13,
01-OCT-2003 (TEMBLFE1. 25,
                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25,
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Q7Z473
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                                                                                                                                                                                                                                                   2 IVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                2 IVWTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIXGASTRATGIPAR 61
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                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                   Query Match 64.7%; Score 363.5; DB 4; Length 109; Best Local Similarity 65.4%; Pred. No. 1.1e-31; Matches 70; Conservative 19; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                           62 FTGSGSATDFTLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                62 FSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
                                                         109 109
109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AA.
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PIR, A32248, A32248.

PIR, B32248, C32248.

PIR, E32530, F32530.

PIR, PH1042, PH1042.

PIR, PH1043, PH1044.

PIR, S07455, S07455.

PIR, S16112, S16112.

PIR, S24501, S24501.

PIR, S24501.

PIR, S24501, S24501.

PIR, S24501.

PIR, S24501, PIR, S24501.

PIR, S24501.

PIR, S24501, PIR, S24501.

PI
  PROSITE, PS50835; IG_LIKE, 1.
NON_TER 10
NON_TER 109
SEQUENCE 109 AA, 11761 MW;
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Best Local Similarity 59.8%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                  SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
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Homo sapiens (Human)
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es 68; Conserva
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NON TER
SEQUENCE
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Q9UL81
ID Q9UL8:
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X MIDINE=22388257; Pubbded=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wadger L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haieh F.,

RA Boares M.B., Bonaldo M.F., Casarant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Paha S.B., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

RA Jones S.J., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                 MEDIINE-98.77139; PubMed=9614934;

M. X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;

Myosin-reactive autoantibodies in rheumatic carditis and normal

fetus.";

Clin Immunol Immunopathol. 87:184-192(1998).

R. PIR, $22638; $23638.

R. PIR, $22638; $23638.

R. InterPro; IPR003596; Ig.v.

R. InterPro; IPR003596; Ig.v.

R. PROSITE; PSS0835; IG_LIKE; I.
                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.5%; Score 357; DB 4; Length 108; Best Local Similarity 60.7%; Pred. No. 5.4e-31; Matches 65; Conservative 21; Mismatches 21; Indels
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA; 11787 MW; DB5845F19724FB4E CRC64;
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Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequ
01-0CT-2003 (TrEMBLrel. 25, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                          108
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                                                                                                                        SEQUENCE FROM N.A.
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                                                                 Mammalia; Euther
NCBI_TaxID=9606;
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NON TER
SEQUENCE
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Q7Z3Y4;
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1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                 23 DIQMIQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82
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Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIK 129
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                                                                                                                                                                                           Query Match 63.5%; Score 357; DB 4; Length 236; Best Local Similarity 62.6%; Pred. No. 1.5e-30; Matches 67; Conservative 19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                  the EMBL/GenBank/DDBJ databases.
Straubberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC005332; AAH05332.1; -.
Hypothetical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 108
108 Aa; 11633 MW; B7BEDC3E41FCCA37 CRC64;
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EMBL; AP035044; AAD56280.1; -.
PIR; PH0863; PH0863.
InterPro; IRBI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA
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SEQUENCE FROM N.A.
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Q8VC55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Score 351.5; DB 4; Length 107; 61.7%; Pred, No. 2.1e-30; ive 20; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE—Colon;

TISSUE—Colon;

Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019760; AAH19760.1; -..
RPIR, A2248; A3248.
RPIR, A33933; A33933.
RPIR; B30577; B30577.
RPIR; B30577; B30577.
RPIR; B30577; B30577.
RPIR; B30577; B30577.
RPIR; B30597; B30577.
RPIR; B31485; B31485.
RPIR; B3248; C3248.
RPIR; C3284; C3248.
RPIR; C3284; C32248.
RPIR; C3287; C27887.
RPIR; C32804; C32887.
RPIR; C32804; C32887.
RPIR; C32804; C32887.
RPIR; D27887; D27887.
                   107 107
107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                     fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035031; AAD56269.1; -.
HSSP; P01607; 1REI.
InterPro: IPR007110; Ig-like.
InterPro: IPR003596; Ig-v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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Matches 66; Conservative
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                                                                                                                                                                                NCBI_TaxID=9606;
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NON TER
SEQÜENCE
                                                                                                     Fragment)
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Q8VCI6;
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Q8VCI6
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Search completed: August 16, 2004, 11:10:29 Job time : 31.6682 secs

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Sequence 167, App
Sequence 167, App
Sequence 53, Appl
Sequence 53, Appl
Sequence 167, App
Sequence 167, App
Sequence 167, App
Sequence 167, App
Sequence 17, App
Sequence 167, Appl
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               Sequence
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Pred. No. 5.4e-45;
3; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: TSO, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIEB/IIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walliam M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
US-08-487-200-3
US-08-487-200-14
US-08-487-200-14
US-08-477-484B-167
US-08-477-584B-85
US-08-477-531B-53
US-08-477-531B-53
US-08-487-560-167
US-08-484-537-14
US-08-411-485-167
US-09-711-485-167
US-09-711-485-167
US-08-428-257A-74
                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/ADENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11823-37-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
                                                                                                                                                                                                                                                                                                          ; Sequence 11, Application US/08458516; Patent No. 5777085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.6%;
Matches 109; Conservative
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amino acid
3Y: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  FOPOLOGY:
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                                                                                                                                                              1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGTLVTVSA 116
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Sequence 3
Sequence 1
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Sequence 1
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(GGDZ 6/ptodata/2/iaa/5B_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/5B_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/6A_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/6B_COMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS CCMB.pep:*
(GGDZ 6/ptodata/2/iaa/PCTUS CCMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-458-516-7

US-08-589-939-1

US-08-589-939-1

US-08-458-516-10

US-08-458-516-12

US-08-458-516-13

US-08-458-516-13

US-08-458-516-13

US-08-458-516-13

US-08-458-516-13

US-08-458-516-13

US-08-458-516-13

US-08-458-516-13

US-08-157-37-65

US-08-918-954-39

US-08-497-312-15

US-08-497-312-15

US-08-50-558E-28

US-08-537-411-11
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US-08-477-728-14
US-08-474-040-3
US-08-474-040-14
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US-08-656-586-4
                                                                                                                                                                                                                            389414 segs, 51625971 residues
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                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                - protein search, using sw model
                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Perfect score:
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Maximum DB
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APPLICANT: Hackett, Jr., John
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61 NEKFKGKATLIVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119
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                                                                            61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: William M. Smith STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-37-3
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11823-37-3
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Patent No. 6111079
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APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSYALDO
APPLICANT: MURRAY, PETER JOSEPH
                                                                                                                                                                                                                                    Sequence 7, Application US/08458516
Patent No. 5777085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
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Best Local Similarity 91.6
Matches 109; Conservative
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US-08-767-128-10
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1 EVQLQQSGABLVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLBWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGP---WFAYWGQGTLVTVSA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLECTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION 925
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATE: 05-JUN-1996
PRIOR APPLICATION DATE: 05-JUN-1996
PRIOR APPLICATION DATE: 06-JUN-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATTER, 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATTER, 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATTER, 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35,093
R: 8648.49USF1
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OOBERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-589-939-1
; Sequence 1. Application US/08589939
; Patent No. 601562
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                            USA
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us-09-889-300a-1.rai

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61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NEKFKCKATLIADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%; Score 503.5; DB 1; Length 119; 80.7%; Pred. No. 3.3e-40; trive 12; Mismatches 8; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: William M. Smith
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
FREFERENCE/DOCKET NUMBER: 11823-37-3
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/ACENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                  APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-458-516-22
; Sequence 22, Application US/08458516
; Patent No. 5777085
                                                                                                                                                                                                                                                                                                     THEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.78
Matches 96; Conservative
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              CURRENT APPLICATION DATA
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CITY: San Francisco
STATE: California
COUNTRY: USA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105
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Patent No. 5777085

GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: To, Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 510.5; DB 3; Length
Pred. No. 8.5e-41;
5; Mismatches 10; Indels
APPLICANT: Hoff, Jane A.
APPLICANT: Ostrow, David H.
APPLICANT: Golden, Alan M.
TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND TITLE OF INVENTION: CONTROLS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   COMPART READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,939
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REPRENCE/DOCKET NUMBER: 5865.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
                                                                                                                                                                        ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: 847-298-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.9%;
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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TELEFAX: 8
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                                                                                                                                                                                                                                                                         COUNTRY:
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Gaps

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61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                        61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLLEWVKQRPGQGL3WIGVINPGSGGTNY
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US-09-157-370-2
US-09-157-370-2
Sequence 2, Application US/09157370A
Patent No. 6262238
GENERAL INFORMATION:
APPLICANT: STEIRE, Boris
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P8341-8072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%; Score 503.5; DB 1; Length 449; 80.7%; Pred. No. 1.4e-39; Live 12; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                                                   APPLICANT: CAN Man Sung
APPLICANT: TSO, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: BILL TO BILL TOWERS: 23
CORRESPONDENCES: 23
ADDRESSEE: ANDIHIGH M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION A24
PRIOR APPLICATION DATA:
APPLICATION TOWNER: US/08/59,159
FILING DATE: 03-MAY-1993
ATTORNEY-AGENT INFORMATION:
NAME: SALACH, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 449 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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96; Conserv
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                                                                                                                                                                             US-08-458-516-13
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Matches 9
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                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                          61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NEKFKGRVTLIVDESTNIAYMELSSLRSEDIAVYFCARRDGNYGWFAYWGQGTLVIVSS 119
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                                                                                                                                                                                                                                                                                                         1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                     DB 1; Length 222;
                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFTCATION: 424
PRICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03.MAY-1993
ATTORNEY/ABOTI INFORMATION:
NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECHONE: 415-326-2400
                                                                                                                                                                                                  82.0%; Score 503.5; DB 1.
80.7%; Pred. No. 6.4e-40;
tive 12; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                     ; LENGTH: 222 amino acids;
TYPE: amino acid
; STRANDEDNESS: single
; TOPOLGGY: linear
; MOLECULE TYPE: protein
US-08-458-516-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: 235 amino acids
amino acid
                                                                                                                                                                                                Query Match
Best Local Similarity 80.75
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80,79
Matches 96; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415-326-2422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-08-458-516-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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9

Gaps

3; Gaps

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1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NEKFKGKATFTADTSSNTAYMQVSSLTSEDSAVYYCARIYYGHLWFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQSGVYELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 78.2%; Pred. No. 5.4e-39;
Matches 93; Conservative 10; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-08-881-037-65
iSequence 65, Application US/08881037
iSequence 1016k, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNB BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Poerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STREET: 755 Page Mill Road
CITY: Palo Alto
STREET: CA
COUNTRY: USA
COMPUTER: EADABLE FORM:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,037
FILING DATE: 23-UNN 1997
CLASSIFICATION NUMBER: US/08/981,037
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: 23,440
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
TELEFAX: (650) 494-0792
                  8648,49USF1
                                                       TELECOMMUNICATION INFORMATION TELEPHONE: 612/371-5278 TELEFAX: 612/332-9081 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO: 65.
SEQUENCE CHARACTER.FATICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internal
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-767-128-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NEKFKGKATLTRDKSSSTAYLQLSSLTSEDSAVYYCARGGYYYFDYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-767-128-20
Sequence 20, Application US/08767128
SEQUENCE OFFECT OFFE OFFE OFFETT OFFTT OFF
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CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-00-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER FILING DATE: 1997-01-14
EARLIER FILING DATE: 1995-00-06
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER PELICATION NUMBER: DE/P44 25 115.7
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY: USA
ZUE: 55402

COMPUTER READALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE: US/08/767,128
FILING DATE: O-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: FILING DATE: 0-DEC-1996
CLASSIFICATION OF 124
PRIOR APPLICATION 1424
PRIOR APPLICATION 0424
PRIOR APPLICATION 0424
PRIOR APPLICATION 0424
PRIOR APPLICATION UNDER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATE:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-UTN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CARTER, Charles G.
REGISTRATION NUMBER: 35,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.3°
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Mus sp.
US-09-157-370-2
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US-07-916-098A-10
Sequence 10, Application US/07916098A
Sequence 10, Application US/07916098A
Parent No. 5871732
APPLICANT: BURKLY, LINDA C.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, MARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NEKFKGKATLIADKSSSTAYMQLSSLISDDSAVYFCARD-----(JPWFAYWGQGTLVTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQQPGAELVKPGASVKLSCKASGYTFSSYWMEWVKQRPGQVL3MIGEINPGNGHTNY 60
                                                                                                                               61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCARD---GPW7AYWGQGTLVTVSA 116
                                                                                                                                                                          61 NEKFKSKATLIVUVKSSSTAYMQLSSLISEDSAVYYCARSFTTARG?AYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLBWIGVINPGSSGGTNY 60
   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGL:3WIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.5%; Score 482; DB 2; Length 122; 72.1%; Pred. No. 3.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALIF BOUGH

CARPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TBM PC COMPACIALISE

CORNETTER: TBM PC COMPACIALISE

SOFTWARE: WORD PERFECT 5.1

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/07/916,098A

FILING DATE: UJY 24, 1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: OT/0591/08843

FILING DATE: NO. 5871732ember 27, 1991

CLASSIFICATION: 424

APPLICATION NUMBER: 07/618,542

FILING DATE: NO. 5871732ember 27, 1990

CLASSIFICATION: 424

APPLICATION NUMBER: 07/618,542

FILING DATE: NO. 5871732ember 27, 1990

CLASSIFICATION: AC DONNELL

REGISTRATION NUMBER: 26,949

REGISTRATION NUMBER: 26,949

REFERENCE/DOCKET NUMBER: 92,310-G

TELECOMMUNICATION NUMBER: 92,310-G

TELECOMMUNICATION NUMBER: 92,310-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: ALLEGRETTI & WITCOFF, LTD.
10 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAN: (312) 715-1200
TELEPAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 10 SOUTH CITY: CHICAGO STATE: ILLINOIS COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 88; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                         61 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARQSYYSYYSWFAYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                      61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-----PWFAYWGQGTLVTVS 115
                                                                                                                                                                                                                                                                                                  1 QVQLLESGAELARPGASVKLSCKASGYTFTSYGISWVKQRTGQGLEWIGEIYPRSGNTYY 60
                                                                                                                                                                                                                                   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08737560A
Patent No. 5928893
GENERAL INFORMATION:
APPLICANT: KANG, Chang-Yuil
APPLICANT: KIM, Joong-Gon
ITILE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
ITILE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: KANG, Chang-Yuil
STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
STREET: KWANAR-GU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
,
                                                                                                   DB 3; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.6%; Score 482.5; DB 2; Length 119; llarity 79.0%; Pred. No. 3e-38; Conservative 8; Mismatches 14; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCUNTRY: Republic of Korea
ZIP: 151-057
ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                               79.1%; Score 485.5; DB 3; Length 1
80.0%; Pred. No. 1.6e-38;
iive 4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: 4B4-1-1 heavy chain variable region US-08-737-560A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: Regula

COUNTY: Regula

ZIP: 135-110

COMPUTER READABLE PORM:

MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage

COMPUTER: IBM PC/AT

COMPUTER: IBM PC/AT

COMPUTER: MS-DSS

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

RPLICATION: NUMBER: US/08/737,560A

FILING DATE: 13-NOV-1996

CLASSIPICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: RR 95-8176
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE:
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LENGTH: 119 amino acids
TYPE: amino acid
                                                                                     Query Match
Best Local Similarity 80.0°
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 94; Conserva
   linear
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STATE: Seoul
COUNTRY: Rep
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US-08-737-560A-10
; TOPOLOGY:
US-08-881-037-65
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: HONG, Hyo Jeong
APPLICANT: HONG, Hyo Jeong
APPLICANT: HONG, Hyo Jeong
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-Yuil
APPLICANT: KANG, Chang-Yuil
APPLICANT: WANG, Chang-Yuil
TITLE OF INVENTION: HYMANICED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
TITLE OF INVENTION: HYMANICAL COMPOSITION COMPRISING SAME
FILE REPERRORCE: 1303-11-12
CURRENT FILING DATE: 1999-11-12
CURRENT FILING DATE: 1999-11-12
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 39
LENGTH: 119
TYPE: PRT
CRAMINE: CRAMINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Variable OTHER INFORMATION: region of heavy chain of mouse monoclonal antibody OTHER INFORMATION: 4B4-1-1 US-09-438-954-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.4%; Score 481.5; DB 4; Length 119; 79.0%; Pred. No. 3.8e-38; Live 8; Mismatches 14; Indels 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/392,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-392-419-2

Sequence 2, Application US/08392419

Sequence 2, Application US/08392419

Patent NO. 5624659

GENERAL INFORMATION:
APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
TITLE OF INVENTION: MITHOD OF TREATMENT

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSED: Renneth D. Sibley
STREET: P.O. Drawer 34009

STATE: Charlotte

STATE: NO. 5624659th Carolina

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,827
FILING DATE: 19-MAR-1993
                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/09438954
Patent No. 6458934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 79.0
Matches 94; Conservative
SA 116
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121 SS 122
                                                                                                                                                                                                                 RESULT 14
US-09-438-954-39
115
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ATTORNEY/ACENT INFORMATION:

NAME: Sibley, Kenneth D.

REGISTRATION NUMBER: 3405-90

TELEPHONE: 919-420-2200

TELEPHONE: 919-420-2200

TELEPHONE: 919-881-3175

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TOPOLOGY: Linear

MOLECULE TYPE: protein
US-08-392-419-2

Query Match

Best Local Similarity 77.1%; Pred. No. 6.18-38;
Matches 91; Conservative 12; Mismatches 13; Indels 2; Gaps

A QVQLOGOSABLVYRPGASVXVSCRASGYAFTNYLLEWVRORPGGGLEWIGYINPGSGGTNY 60

I QVQLOGOSABLVYRPGASVXVSCRASGYTFTSYVTHWVRORPGGGLEWIGYINPGSGGTNY 79

TO EVQLOGOSABLVYRPGASVXVSCRASGYTFTSYVTHWVRONPGGGLEWIGYINPFNDGTXY 79

OF THE LOCAL SIMILARITY AND THE SELFTSESSAVYFCARD GFOREWIGYINPENDGTXY 79

OF THE LEGAL STATE TO THE SELFTSESSAVFCARDMGREGFAYMGGGTLWTVSA 137

Search completed: August 16, 2004, 11:12:57
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us-09-889-300a-1.rapb

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August 16, 2004, 11:10:36 ; Search time 42.1345 Seconds (without alignments) 864.269 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEp:*

3: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEp:*

4: \cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_pep:*

7: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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10: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

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13: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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16: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

17: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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11: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

13: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1292805 seqs, 313927144 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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614
                                 Copyright
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appl	Appli	Appl	Appl	Appl	Appl	Appl								
		54,	54,	54,	54,	54,	54,	54,	54,	54,	80	53,	53,	53,	53,	53,
	Description	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence
	ΙD	US-10-411-037-54	US-10-411-026-54	US-10-410-962-54	US-10-411-049-54	US-10-410-930-54	US-10-410-997-54	US-10-411-012-54	US-10-287-994-54	US-10-410-913-54	US-10-146-305-8	US-10-411-037-53	US-10-411-026-53	US-10-410-962-53	US-10-411-049-53	US-10-410-930-53
	DB	12	12	16	16	16	16	16	16	16	13	12	12	16	19	16
	Query Match Length	119	119	119	119	119	119	119	119	119	138	119	119	119	119	119
,de	Query Match	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	84.5	82.0	82.0	82.0	82.0	82.0
	Score	554.5	554.5	554.5	554.5	554.5	554.5	554.5	554.5	554.5	519	503.5	503.5	503.5	503.5	503.5
	Result No.		7	٣	4	ഹ	9	7	ω	თ	10	11	12	13	14	15

TYPE: PRT
) ORGANISM: Mus musculus
US-10-411-037-54

Appl	Appl	Appl	Appl	App1	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appli	Appli	Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appli
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Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence						
-10-410-997-5	10-411-012	-10-287-994-5	-10-410-913-5	-10-411-037-5	-10-411-026-5	-10-410-962-5	-10-411-049-5	-10-410-930-5	-10-410-997-5	-10-411-012-5	-10-287-994-5	-10-410-913-	-307-276B-	-10-006-773-	-10-435-614-1	-10-435-614-	-10-435-614-	-10-435-614-2	10-307-2	-10-307-276B-	-10-447-257-	-10-010-729	-10-467-546-	-10-467-546-	10-153-024-	-10-360-053-	-10-360-0	10-307-276B	US-10-460-595-5
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	Chen,
; APPLICANT: Chen, Xi	Hakes,
Hakes, Chen, X	Bayer,
Bayer, Hakes, Chen, X	Zopf,
Zopf, D Bayer, Hakes, Chen, X	
	Neose Technologies,
Neose Technologies, DeFrees, Shawn Zopf, David Bayer, Robert Hakes, David Chen, Xi	ORMATION:
ORNATION: Neose Technologies, DeFrees, Shawn Zopf, David Bayer, Robert Hakes, David Chen, Xi	
Sequence 54, Application US/10411037 Publication No. US20040043446A1 GENERAL INFORMATION: APPLICANT: Neose Technologies, Inc. APPLICANT: DeFrees, Shawn APPLICANT: Depf. David APPLICANT: Bayer, Robert APPLICANT: Hakes, David APPLICANT: Hakes, David	ት ት ት

ALIGNMENTS

APPLICANT: Bowe, Caryn
TITLE OF INVENTION: ALEACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: ALEACTOSIDASE A
FILE DET INVENTION: ALEACTOSIDASE A
FILE OF INVENTION: ALEACTOSIDASE A
FRIOR PELLING DATE: 2001-10-10
FRIOR FILING DATE: 2001-10-10
FRIOR FILING DATE: 2002-06-25
FRIOR FILING DATE: 2002-06-26
FRIOR FILING DATE: 2002-06-26
FRIOR FILING DATE: 2002-08-28
FRIOR FRIOR PROPERTION NUMBER: US 60/407,527
FRIOR FRIENCE PROPERTION NUMBER: US 60/407,527
FRIOR FILING DATE: 2002-08-28
FRIOR FRIOR PROPERTION NUMBER: US 60/407,527
FRIOR FRIOR FRIOR PROPERTION NUMBER: US 60/407,527
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APPLICANT: acgl. David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
ITILE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYJOCONJUGATION OF INTERFERO
FILE REFERENCE: 040833-01-505
CURRENT APPLICATION NUMBER: US/10/411,049
FRICK APPLICATION NUMBER: US 60/326,523
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR PRILING DATE: 2002-06-07
PRIOR PRILING DATE: 2002-06-07
PRIOR PRILING DATE: 2002-06-07
PRIOR PRILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
             APPLICANT: Hakes, Desci-
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
FILE REPERENCE: 04063-01-5054
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR PELING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR PRILING DATE: 2002-06-25
PRIOR PRILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR PRILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
PRIOR PRILING DATE: 2002-06-26
PRIOR PRILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEKFKGKATLIVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGW?AYWGRGTLVIVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
Bayer, Robert
Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-10-410-962-54
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US-10-411-049-54
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Publication No. US20040063911A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Copf. David
APPLICANT: Bayer. Ched. Xi
ITLE OF INVENTION: WETHOOS
FILE OF INVENTION: WETHOOS
FILE OF INVENTION: WETHOOS
FILE OF INVENTION: WHORER: US/10/411,026
CURRENT FILING DATE: 2001-010
PRIOR APPLICATION NUMBER: US 60/328,533
PRIOR PLILNG DATE: 2001-10-10
PRIOR PAPLICATION NUMBER: US 60/344,692
PRIOR PLILNG DATE: 2001-10-10
PRIOR PLILNG DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PLILNG DATE: 2002-06-07
PRIOR PLILNG DATE: 2002-06-07
PRIOR PLILNG DATE: 2002-06-05
PRIOR PLILNG DATE: 2002-06-05
PRIOR PLILNG DATE: 2002-06-05
PRIOR PLILNG DATE: 2002-06-05
PRIOR PLILNG DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-16
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PRIOR PLING DATE: 2002-06-16
PRI
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                                         DB 12;
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                                     Query Match
90.3%; Score 554.5; DB 17
Best Local Similarity 91.6%; Pred. No. 1.8e-45;
Matches 109; Conservative 3; Mismatches 4
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91.6%; Pred. No. 1.8e-45;
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Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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Matches 109; Conservative
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CAGANISM: Mus musculus
US-10-411-026-54
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TITE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF TITLE OF INVENTION: FSH.

FILE OF INVENTION: FSH.

FILE OF INVENTION: FSH.

CURRENT APPLICATION NUMBER: US (10/410,997

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: US 60/324,692

PRIOR PILING DATE: 2001-10-10

PRIOR PILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-08-16

PRIOR PRIOR DATE: 2002-08-16

PRIOR PRIOR DATE: 2002-08-16

PRIOR PRIOR DATE: 2002-08-16
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APPLICANT: DeFrees, Shawn
APPLICANT: Doff, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bower, Caryne
TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
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Pred. No. 1.8e-45;
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CURRENT APPLICATION NUMBER: US/10/411,012
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
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Publication No. US20040132640A1
GENERAL INFORMATION:
                                                                                                                                                  Sequence 54, Application US/10410997
Publication No. US20040126838A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
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91.6%;
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Best Local Similarity 91.6<sup>3</sup>
Matches 109; Conservative
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Zopf, David
Bayer, Robert
Hakes, David
Chen, Xi
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; ORGANISM: Mus musculus
US-10-410-997-54
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US-10-411-012-54
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: According to the control of the control 
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Pred. No. 1.8e-45;
3; Mismatches 4
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91.6%; Pred. No. 1.86
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 54
LENGTH: 119
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Publication No. US20040115168A1
GENERAL INFORMATION:
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APPLICANT: DeFrees, Shawn
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91.6%;
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Best Local Similarity 91.65
Matches 109; Conservative
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Best Local Similarity 91.6:
Matches 109; Conservative
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; ORGANISM: Mus musculus
US-10-410-930-54
                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mus musculus
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-10-410-913-54
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Matches
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APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Caryn
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, NUMBER: US/10/287,994
CURRENT APPLICATION NUMBER: US/00/287,994
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-60-7
PRIOR FILING DATE: 2002-60-7
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-60-7
PRIOR FILING DATE: 2002-60-16
PRIOR FILING DATE: 2002-60-18
PRIOR FILING DATE: 2002-08-16
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           PRIOR AFFLATION TOWNER: US 60/387,292
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 54
LENGTH: 119
PRIOR APPLICATION NUMBER: US 60/344,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 54, Application US/10287994
Publication No. US20040137557A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Neose Technologies, Inc
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91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-012-54
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; ORGANISM: Mus musculus
US-10-287-994-54
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Best Local Similarity
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer Robert
APPLICANT: Bayer Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, X1
APPLICANT: Bowe, Caryn
ITILE OF INVENTION: GIYCOCOJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
ITILE OF INVENTION: METHORS: US 6/320,203
FILE REFERENCE: 040853-01-5081
CURRENT FILING DATE: 2001-10-10
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/387,292
PRIOR PAPLICATION NUMBER: US 60/391,777
PRIOR PAPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTHARE: PATENTING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTHARE: PATENTING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
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Sequence 8, Application US/2020173035A1
GENERAL INFORMATION:
APPLICANT: YUHAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
FILE REFERENCE: CV17440
CURRENT APPLICATION NUMBER: US/10/146,305
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                                                                                                                                          1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 60
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3; Gaps
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4; Indels
3; Mismatches
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Best Local Similarity 91.69
Matches 109; Conservative
109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Mus musculus
US-10-410-913-54
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1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60
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82.0%; Score 503.5; DB 12; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                                                                                               ; Sequence 53, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-53
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US-10-410-962-53
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Sequence 53, Application US/10411037

Publication No. US20040043446A1

Sequence 53, Application US/10411037

Publication No. US20040043446A1

APPLICANT: Newer Percentages, Inc.

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Sobyid

APPLICANT: Where I do (1972)

TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA

TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA

TITLE OF INVENTION: GALACTOSIDASE

TITLE OF INVENTION NUMBER: US 60/326,523

PRIOR APPLICANTION NUMBER: US 60/326,523

PRIOR APPLICANTION NUMBER: US 60/391,777

PRIOR FILING DATE: 2002-06-07

PRIOR PLING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR APPLICANTION NUMBER: US 60/404,249

PRIOR APPLICANTION NUMBER: US 60/407,327

NUMBER OF SEQ ID NOS: 75

SEQ ID NOS: 75

SEQ ID NOS: 75

SEQ ID NO S3

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                                                                                                                                                                                                                                                                                                                                                                                        Score 519; DB 13; Length 138;
Pred. No. 5.3e-42;
5; Mismatches 9; Indels
       ; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION WUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentin 1.71
; SOFTWARE: ROPATH: 138
; LENGTH: 138
; TYPE: PRT
; CRGANISM: Escherichia coli
US-10-146-305-8
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.6%;
Matches 102; Conservative
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|:
121 SS 122
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APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Dorive Control Co 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116 Sequence 33. Application US/10410962

Publication No. US2004007783641

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bower, Caryn
APPLICANT: Green, Xi
APP 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116 61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119 1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY Gaps

us-09-889-300a-1.rapb

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APPLICANT: Defice b, sucari,
APPLICANT: Lower b, sucari,
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMOBELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: BETA
FILE REFREENCE: 040853-01-5056
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
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                                                                                                                                                              DB 16; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.0%; Score 503.5; DB 16; Length 119; Best Local Similarity 80.7%; Pred. No. 1.4e-40; Matches 96; Conservative 12; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                       .4e-40;
                                                                                                                                                         Query Match
Best Local Similarity 80.7%; Pred. No. 1.4e
Matches 96; Conservative 12; Mismatches
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Job time : 43.1345 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-410-930-53
; Sequence 53, Application US/10410930
; Bublication No. US20040115168A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Neose Technologies, Inc. APPLICANT: DeFrees, Shawn APPLICANT: Zopf, David APPLICANT: Bayer, Robert APPLICANT: Hakes, David
                           ; ORGANISM: Homo sapiens
US-10-411-049-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-410-930-53
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APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Eder, Xi
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Bowe, Cary
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: LALPHA
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: UNMBER: US 60/328,53
PRIOR PLING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/404,24
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR PRIOR PRIOR DATE: 2002-08-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.0%; Score 503.5; DB 16; Length Best Local Similarity 80.7%; Pred. No. 1.4e-40; Matches 96; Conservative 12; Mismatches 8; Indels
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR PLLING DATE: 2003-04-09
PRIOR PLLING DATE: 2001-10-10
PRIOR PLLING DATE: 2001-10-19
PRIOR PLLING DATE: 2001-10-19
PRIOR PLLING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR PLLING DATE: 2002-06-07
PRIOR PLLING DATE: 2002-06-07
PRIOR PLLING DATE: 2002-06-15
PRIOR PLLING DATE: 2002-06-15
PRIOR PLLING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
SOCTWARRE: PRECEIL VERFAION 3.2
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Sequence 53, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-410-962-53
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GenCore version 5.1.6
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August 16, 2004, 11:08:06; Search time 12.4843 Seconds (without alignments) 893.780 Million cell updates/sec US-09-889-300A-1 614 1 QVQLQQSGAELVRPGTSVKV......ARDGPWFAYWGQGTLVTVSA 116 OM protein - protein search, using sw model Run on:

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	q heavy chain V	g heavy	g heavy chain V	g he	L7-6 antibody he	P T	g q	g heavy chain	g heavy	g heavy chain V	g heavy chain V	q qamma chain -	þ	g heavy chain V	q heavy chain pr	chain V	g heavy chain pr	q heavy chain V	g heavy chain V	g heavy	g heavy chain pr	g heavy chain v	g heavy chain pr	q heavy chain V-	ntibody Fab	g heavy chain V-			
	ID	B30560	in	320640	A30577	JC2269	C30562	G2MS11	F29380	C30560	S38565	S21810	838950	840295	E30562	JL0076	D30562	E29380	A27472	809216	HVMST7	37	148	α	167	9	VMSG	9660	853751	4867
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RESULT 2
S60067

19 heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragment C) globes. Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C; Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C; Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
R; Mich. M. Filman, D. J; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogl-Nat. Structure of the complex between the fab fragment of a neutralizing antibody fragment connection 10-00067
A; Michael Complex S60066; MUID:95292109; PMID:7539711
A; Molecule type: mRNA
A; Mesidues: 1-123 *WIED
A; Residues: 1-123 *WIED
A; Residues: 1-123 *WIED
A; Cross-references: EMBL: R84698; NID:9773225
R; Wien, M.W.; Hogle, J.M.

heavy chain	heavy chain	heavy chain	heavy chain	pelB leader/Ig hea	heavy chain	heavy chain	heavy chain	chain		heavy chain		heavy chain	heavy chain	heavy chain	Ig heavy chain V r
A30502	825176	MHMS18	A39276	PC4402	PL0232	819969	538717	B22769	866537	F48677	E32513	A56700	S55542	837201	G28195
2 A30502		-	-	4 PC4402			2 \$38717		2 \$66537		2 E32513				2 G28195
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112 2	117 2	139 1 1	141 2	4	112 2	121 2	118 2	120 2	131 2	123 2	138 2	115 2	116 2	N	9 120 2 (
112 2	117 2	139 1 1	75.9 141 2	287 4	112 2	75.8 121 2	75.7 118 2	120 2	131 2	75.5 123 2	138 2	75.3 115 2	75.3 116 2	9 118 2	74.9 120 2 (

ALIGNMENTS

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Gaps

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PUT-6 antibody heavy chain - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Was musculus (house mouse)
C; Dates: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C; Accession: J02269; PC2186
R; Kurome, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kamihagi, K.; Yasumoto, M.; Ka
J; Title: Expression of recombinant mouse/human chimeric antibody specific to human GM
A; Reference number: JC2269; MUID:94334310; PMID:7520038
A; Mccession: JC2269
A; MID:9434310; PMID:7520038
A; Mccession: JC286
A; Mccession: PC2186
A; Mccession: McCession: Millian A; Residues: 2-27 kML2>
A; Experimental source: hybridoma cell
C; Comment: This protein is specific to human P-selectin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 2-98/Region: immunoglobulin homology < IMM>
C; Mccession: Immunoglobulin homology < IMM>
C; Mccession: McCession: Immunoglobulin homology < IMM>
C; Mccession: McCession: Immunoglobulin homology < IMM>
C; Mccession: McC
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(230562
Ig heavy chain V region (27.7.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996.
C;Accession: (230562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, T. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen A;Reference number: A30562; MUDD:89110066; PMID:2464031
A;Accession: (230562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 cSIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWIGNIYPGSSSTNY 79
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              Length 135;
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                                                                                                            16;
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                  Score 491; DB 2;
Pred. No. 1.7e-37;
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80.0%; SCOLL NO. 1.7e-282.8%; Pred. No. 1.7e-2
                                                                                                            96; Conservative
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F;107-117/Region: J segment
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Matches 92
                       Query Match
Best Local S:
Matches 96
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C.Species: Mus musculus (house mouse)
C.Species: Was musculus (house mouse)
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C.Accession: 820640, $20644
R.Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
Submitted to the BMBL Data Library, February 1992
A.Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A.Reference number: 820639
A.Accession: 820640
A.Status: preliminary
A.Mocession: 820640
A.Status: preliminary
A.Mocession: 820640
A.Status: preliminary
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology <LWM>
C.Superfamily: immunoglobulin homology <LWM>
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Javovi,
Javovi,
Javovi,
Javovi,
Javovi,
Javovi,
Jahary chain precursor V region (MRLIO) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A30577
R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof
R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela
A;Reference number: A30577
A;Accession: A30577
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NANFKGKATLTADKSSSIVYMQLSSLTSDDSAVYFCARDFYDYDVGFDYMGQCTTLTVSS 120
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              submitted to the Brookhaven Protein Data Bank, January 1995
A;Reference number: A52979; PDB:1FPT
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-123
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology atmworfs: P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;22-96/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIQWIKQRPGQGLEWIGVINPGSGGTDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 526; DB 2; Length 12.
Pred. No. 1.1e-40;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.7%;
Best Local Similarity 85.0%;
Matches 102; Conservative
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Best Local Similarity 77.34
Matches 92; Conservative
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igheavy chain precursor V region (A003 40/5G7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: F29380
C;Accession: F29380
C;Accession: F29380
A;Chen, Hr.T; Kabat, B.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable A;Reference number: A92612; MUID:88007582; PMID:3115981
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                                           F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220.288-344,394-452/Disulfide bonds: #status predicted
F;247_250.283-356/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 EVQLQQSGPELVNPGASVKASCKASGYTFITVVAHWYKQKPGQGLEWIGYINPNKDGTKF 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (35.8.2H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
C;Accession: C30566
C;Accession: C30566
C;Accession: C30566
C;Accession: L3A
J:Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of m
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-118 <AMAT>
A;Cross-references: GB:M24270; NID:g195615; PIDN:AAA38371.1; PID:g195616
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 487; DB 1; Length 474; 77.1%; Pred. No. 1.5e-36; ive 11; Mismatches 14; Indels
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Pred. No. 6.1e-37;
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F;157-222/Domain: immunoglobulin homology <IMl>
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Best Local Similarity
Matches 94; Conserv
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A; Residues: 1-137 < CHE>
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A,Residues: 138-172, 'P',174-189,'FP',193-376,'T',378-474 <TU2>
A,Molecule type: DNA
A,Residues: 138-172, 'P',174-189,'FP',193-376,'T',378-474 <TU2>
R,Ollo, R.; Rougeon, P.
Nature 296, 761-763, 1982
A,Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma, A,Reference number: A26233
A,Molecule type: DNA
A,Cossion: A2633
A,Molecule type: DNA
A,Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A,Cors-references: GB:000461
A,Residues: 138-161,'L',Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
A,Cossion: A535-12350, 1994
A,Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A,Reference number: A53598, MUD:94216359; PMID:7512967
A,Reference number: A53598, MUD:94216359; PMID:7512967
A,Residues: 234-251 <KIM>A,Residues: 234-251 <KIMANDOJObulin heterotetramer: immunoglobulin heterotetramer; immunoglobulin heterotetramer; immunoglobulin heterotetramer; immunoglobulin heterotetramer; immunoglobulin heterotetramer; immunoglobulin heterotetramer;
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S26057; A02157; A26235; A26232; A26233; A353598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific A;Reference number: S25057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleoride sequence of immunoglobulin gamma2b chain gene cloned from A,Reference number: A02157; MUID:80120716; PMID:6766534
    61 NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARHYYGSSSFAYWGQGTLVTVSA 119
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A,Molecule type: mRNA
A,Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A,Note: Lys-474 is probably removed posttranslationally
R,Tucker, P.W.; Marcu, KB.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A,Title: Sequence of the cloned gene for the constant region of murin
A,Reference number: A26232; MUID:80081502; PMID:117549
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A; Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A; Cross-references: GB:J00461
A; Note: the sequence was determined from the germline gene
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A; Tille: Structure of the constant and 3' untranslated regions
A; Reference number: A26235; MUID:80081501; PMID:117548
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-474 <FIS>
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us-09-889-300a-1.rpr

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Iggamma chain - mouse
[Gramma chain - mouse
[Gramma chain - mouse
[Gramma chain - mouse]
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A;Description: Primary structure of the murine monoclonal IgGza antibody mAb735 again: A;Reference number: S40295
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                                                                                         NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARNYGSSYGLAYWQQGTLVTVSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Map position: 12
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NEKFKGKATITADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NEKFKGKATLIVDISSSTAYMQLSSLISEDSAVYFCARGGKFAMDYWGQGISVIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQSGABLVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY
                                                  NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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File-1446/Domain: C region <CHN>
File-214/Domain: C1 region <CH1>
File-214/Domain: C2 region <CH2>
File-214/Domain: C2 region <CH2>
File-246/Domain: C2 region <CH3>
File-446/Domain: C3 region <CH3>
File-446/Domain: C3 region <CH3>
File-446/Domain: C3 region <CH3>
File-446/Domain: G3 region <CH3>
File-446/Domain: G3 region <CH3>
File-419/Domain: immunoglobulin homology <IMM>
File-419/Domain: immunoglobulin homology <IMM>
File-419/Domain: immunoglobulin homology <IMM>
File-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
File-324,227,229/Disulfide bonds: interchain #status predicted
File-347/Binding site: carbohydrate (Asn) (covalent) #status experimental
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C,Superfamily: immunoglobulin C region; immunoglobulin homology C,Keywords: immunoglobulin
C,Keywords: immunoglobulin
F,137-201/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.6%; Score 482.5; DB 2
79.5%; Pred. No. 1.9e-36;
iive 7; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.5e-36; 7; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 482.5;
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79.5%;
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Best Local Similarity 79.53
Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S40295
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Igheavy chain V region - mouse

C,Species: Meb-1995 #text_change 23-Jul-1999

C;Bate: 20-Feb-1995 #text_change 23-Jul-1999

C;Bate: 20-Feb-1995 #text_change 23-Jul-1999

C;Catession: S21810

R;Ostermeyer, M.; Brack, C.H.; Trauncker, A.; Koehler, G.

R;Ostermeyer, M.; Brack, C.H.; Trauncker, A.; Koehler, G.

R;Ostermeyer, M.; Brack, C.H.; Trauncker, A.; Koehler, G.

R;Ostermeyer, M.; Brack, C.H.; Trauncker, January 1991

A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha

A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha

A;Description: S21810

A;Accession: S21810

A;Accession: S21810

A;Accession: S21810

A;Status: DNA

A;Residues: DNA

A;Residues: DNA

A;Residues: 1-138 <CST>
A;Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164

A;Introns: 15/3

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin

E;34-117/Domain: immunoglobulin homology <INM>
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R. Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A. Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s ?
A. Reference number: S3859
A. Status: preliminary
C. Superfement: EMBL: X75100; NID: 914157; PIDN: CAA52991.1; PID: 9414158
C. Suberfementy: immunoglobulin V region; immunoglobulin homology
C. Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                              61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                         61 NEKFKGKATLITADKSSSTAYMQLSSLTSDDSAVYFCARDGP---WFAYWGQGTLVTVS 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J heavy chain V region (ASWV1) - mouse (fragment)
Species: Mus musculus (house mouse)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                                                 Gaps
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           Length 118
78.8%; Score 484; DB 2; Length 11 78.0%; Pred. No. 6.4e-37; ive 10; Mismatches 14; Indels
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79.8%; Pred. No. 8.4e
:ive 7; Mismatches
                                                                         92; Conservative
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Best Local Similarity 79.8
Matches 95; Conservative
Query Match
Best Local Similarity
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80 NEKFKSKATLIVDKPSSTAYMQLSSLISEDSAVYYCAREGPAGDYWGQGTTLIVSS 135
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ne : 13.4843 secs
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R. Sikder, S. K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A. Timmunol. 142, 888-893, 1989
A. A. A. Cession: E30562
A. R. Sikderence number: A30562; MUD: 89110066; PMID: 2464031
A. Reference number: A30562; MUD: 89110066; PMID: 2464031
A. Reference number: A30562
A. Settus: preliminary
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: heterotetramer; immunoglobulin homology < INMA
F:15-98/Domain: immunoglobulin homology < INMA
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R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Titlele: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
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61 NEKFKGKATLIADKSSSTAYMQLSSLISDDSAVYFCAR---DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                  B30562
Ig heavy chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
                                                                                                             61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
                                                                                                                                                         61 NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSS 117
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A,Residues: 1141 «KAA»
A,Residues: 1141 «KAA»
A,Cross-raferences: 0812/788; NID:g195851; FIDN:AAA38441.1; PID:g195852
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted «SIG»
F;20-141/Product: Ig heavy chain #status predicted «MAT»
F;34-117/Domain: immunoglobulin homology «IMM»
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C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted
F;20-141/Product: Ig heavy chain #status predicted
F;34-117/Domain: immunoglobulin homology <IMM>
F;05-54/Region: complementarity-determining 1
F;69-56/Region: complementarity-determining 2
F;123-135/Region: C
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MEDLINE=84248078; PubMed=6429663;
A Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
A Tucker P.W.;
Tullegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
Horo. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
RISP; PO1810; 2FBJ.
RISP; PO1810; 2FBJ.
RISP; PO1810; 2FBJ.
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23-OCT-1986 (Rel. 02, Last sequence update)
15-UL-1996 (Rel. 02, Last snotation update)
15-UL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region TEFC 1017 precursor.
Buk musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Sciurognathi; Muridae; Musinae, M
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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HV39 MOUSE
HV30 MOUSE
HV16 MOUSE
HV3K HUMAN
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
                                                                                                                                                                                                                                                                                                                                         US-09-889-300A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SwissProt 42:*
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4601.5
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Maximum DB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 EKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD-----GPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYYFDYWGQGTTLTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
                                                                                                                                                                                                                                                            "The generic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

Bur. J. Immunol. 12:1023-1032[1982].

-!- MISCELLANEOUS: FROM MANUASIS OF THE SIZES OF SEVERAL OFHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME CONCLUDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.8%; Score 471.5; DB 1; Length 120; 76.7%; Pred. No. 1.4e-42; ive 8; Mismatches 15; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                         SEGMENT, JH2.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP, P01789; IMCP.
InterPro; IPR07110; IG-like.
InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin heavy Chain.";
Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILNE=81131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region 93G7 precursor.
                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 36-65.
120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1. ...
SMART; SMO4066; IGV; 1. SPAGTE; PS50835; IG LIKE; 1. Immunoglobulin V region; Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A/J;
MEDLINE=82152818; PubMed=6801765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92; Conservative
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 STANDARD;
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120 AA;
                                                                                      Ig heavy chain V reg
Mus musculus (Mouse)
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                                                                                                                                                         NCBI_TaxID=10090;
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 HV03 MOUSE
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HV02_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD----GPW-FAYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQSGABLVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANBOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baltimore D.; "Heavy chain variable region contribution to the NPb family of
                                                                                                                                                                                                                                                                                                                    76.5%; Score 469.5; DB 1; Length 140; 76.9%; Pred. No. 2.7e-42;
                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION 93G7.
IG-LIKE.
                                                                                                                                                                                                                                                                                         15514 MW; 25A4CBBE31DASCE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POI751; POI752,
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11g heavy chain V region B1-8/186-2 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 A.A.
                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                            EMBL, J00493; AAA38128.1; -.
PIR; A94264; HVMSG7.
HSSP, PO1810, 2FBJ.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_v.
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                                                                                                                                                                                                                                                                                                                                                       93; Conservative
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139
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                                                                                                                                                                                                                                                                        140 AA;
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                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              80 NEKFKSKATLITUDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR----DGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981)
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOWA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                                                                                                                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                                                                                                                                                                                                                                                                            1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                  Gaps
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                        IG HEAVY CHAIN V REGION B1-8/186-2.
                                                                                                                     FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                      75.9%; Score 466; DB 1; Length 139; 74.2%; Pred. No. 6.3e-42; ive 11; Mismatches 16; Indels
                                                                                                                                                            COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                            15419 MW; 1B57DD4FD0C9F465 CRC64;
PDB; 1A6W; 15-JUL-98.
InterPro; IRRO07110; 1g-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGv.
IRRUPOSTER; PS50835; IG LIKE; 1.
IRRUNOG10bulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 843 precursor.
                                                                                                                                                                                        D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
                                                                                                                                                                          FRAMEWORK-3.
                                                                                                                                                   FRAMEWORK-2
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00539; AAA38172.1; -.
PIR; A02038; G2MS43.
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                (NPB ANTIBODIES)
                                                                                                                                                                                                                                            139 AA;
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                                                                                                                                                                                                                                                                                      Similarity
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DOMAIN
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SEQUENCE
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Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains.";
Biochemistry 21:5415424(1982).
---- MISCELLANBOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                        QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASM-55.
MEDLINE-83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                2
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.2%; Score 455.5; DB 1; Length 117; larity 73.5%; Pred. No. 6.5e-41; Conservative 14; Mismatches 16; Indels 1
                                                                           COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                      Length 137;
                                       CHAIN V REGION S43
                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 96 BY SIMILARITY.
55 55 N-LINKED (GLCNAC. . .) (CC
117 117
117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
                                                                                                                                                                                                                                              15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02039; MHMS4E.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                      74.4%; Score 457; DB 1; 73.7%; Pred. No. 5.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-GCT-2003 (Rel. 42, Last annotation update)
11g heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA
                                                                                                                                                                                                                                                                                                                                12; Mismatches
                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                             FRAMEWORK-3.
                                                                                                                                                                                     SEGMENT
                                     IG HEAVY CH
FRAMEWORK-1
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                                                                                                                                                               D SEGMENT
region; Signal
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.7'
Matches 87, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                       41
137
137 AA;
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86; Conserv
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Matches 86
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61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR-----DGPWFAYWGQGTLVTVS 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=84182519; PubMed=6201362;
Dildfrop R., Bovens V., Slekevitz M., Beyreuther K., Rajewsky K.;
Dildfrop R., Bovens V., Slekevitz M., Beyreuther K., Rajewsky K.;
A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
EMBO V. 3:517-523(1984).
PIR, A02037; MHMS15.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                 / Match 74.0%; Score 454.5; DB 1; Length 121; Local Similarity 71.9%; Pred. No. 8.7e-41; les 87; Conservative 11; Mismatches 18; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
                                                                                                                                                                                                                                                                        121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
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105 D SEGMENT.

120 J SEGMENT.

96 BY SIMILARITY.

120

13311 MW, 914453F426F09834 CRC64;
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Pred. No. 2e-38;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
IG heavy chain V region AC38 15.3.
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Res. 8:3591-3601(1980)
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; IJ_
SWART; SW00406; IGv; I,
PROSITE; PSS0835; IG_LKE; I.
Immunoglobulin V region.
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22
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120 AA;
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Best Local Similarity
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Nucleic Acids
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P06329;
                              REVISIONS.
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SEQUENCE
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us-09-889-300a-1.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523 (1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLQQSGABLVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
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                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEAVY CHAIN V REGION VH558 A1/A4.
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                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-8509340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
Tewerlopmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION VH558 PERAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 427; DB 1;
Pred. No. 6.4e-38;
neavy chain V region VH558 Al/A4 precursor.musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 205.12.
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PIR; A02029; HVMSA1.
HSSP; PO1810; 2FBJ.
INTERPRO; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
SIGNAL
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83.7%;
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82; Conserv
                                                                                                     NCBI_TaxID=10090;
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P06330;
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SEQUENCE
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Best Local
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HV51_MOUSE
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                                                      QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                     1 OVOLLOPGTELVKPGASVNLSCKASGYTFTSYWMHWIRORPGOGLEWIGGINPSNGGTNY
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     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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COMPLEMENTARITY-DETERMINING-1.
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     20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION 23.
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81.6%; Pred. No. 3.9e-38;
iive 7; Mismatches 11;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 23 precursor.
     13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
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nes 80; Conservative
     83; Conservative
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85
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117 1
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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01-JAN-1988
15-JUL-1999
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P01748;
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HV52_MOUSE
ID HV52 MC
AC P06327;
DT 01-JAN-
DT 15-JUL-
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61 NEKFKGKATLTADKSSTAYMQLSSLTSDDSAVYFCAR 98
                                                                                            67.4%; Score 414; DB 1;
79.6%; Pred. No. 1.5e-36;
iive 8; Mismatches 12;
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SMARI, SM00406; iGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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Best Local Similarity
Local 78; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NEKFKGKATLIADKSSSTAYMQLSSLTSDDSAVYFCARDGPW--FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heavy chain, variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                               Gaps
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Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECALLANCOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

PIR, A02031; HWAS02.

HSSP; PO1810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR007319; Ig-like.

Ffam; PF00047; ig: 1.

SMART; SM00406; IGV; 1.

FMART; SM00406; IGV; 1.

Immunoglobulin V region; Signal.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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81.2%; Pred. No. 1.5e-36;
ive 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                        69.2%; Score 425; DB 1; Length 118; 68.6%; Pred. No. 1e-37; ive 14; Mismatches 21; Indels
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                             105 118 J SEGMENT.
22 96 BY SIMILARITY.
118 118 118 W, 94F7BEB4C762A018 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
119 heavy chain V region 102 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA
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BY SIMILARITY.
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PIR; A02040; MHMS38.
HSSP; P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
PROSITE; PS00406; IG-LIKE; 1.
PROSITE; PS50835; IG-LIKE; 1.
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Best Local Similarity 81.2
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                          Local Similarity 68.6 es 81; Conservative
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118
96
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117 AA;
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                          21 VQLQQPGAELVKPGASVKVSCKASGYTFTSYWAHWVKQRPGQGLEWIGRIHPSDSDINYN 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWYKQRPGRGLEWIGRIDPNSGGTKY 79
2 VOLOQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNYN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                     HV09_MOUSE STANDARD; PRT; 117 AA.
P01753; P11271;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
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54 COMPLEMENTRITY-DETERMINING-
68 COMPLEMENTARITY-DETERMINING-
85 COMPLEMENTARITY-DETERMINING-
117 FRAMEWORK-3.
118 BY SIMILARITY.
117
117
11890 MW, 16191A088CB17F5A CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-!- MISCELLANBOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                       MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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Best Local Similarity 79.6%; Pred. No. 3e-36;
Matches 78; Conservative 9; Mismatches 11; Indels
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MGD; MGT: 96466, IGH-VJ558.
InterPro; IPR007110; IG-like.
InterPro; IPR003596, IG-V.
Ffam, PP00047; ig; 1.
FROMI; SM00406, IGV; 1.
PROSITE; PS50835; IGLIKE; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             Baltimore D.;
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Gaps

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Search completed: August 16, 2004, 11:08:35 Job time: 8.32287 secs

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ŏ	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	
OM protein - protei	protein search, using sw model	
Run on: Augi	August 16, 2004, 11:08:06; Search time 34.3318 Seconds (without alignments) 1066.069 Million cell updates/sec	
Title: US-(Perfect score: 614 Sequence: 1 Q	US-09-889-300A-1 614 1 QVQLQQSGAELVRPGTSVKVARDGPWFAYWGQGTLVTVSA 116	
Scoring table: BLOS Gapo	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched: 1017	1017041 segs, 315518202 residues	
Total number of hits	s satisfying chosen parameters: 1017041	
Minimum DB seq lengt Maximum DB seq lengt	length: 0 length: 200000000	
Post-processing: Minimum Match Maximum Match Listing first	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : SP: 1: 12: 2: 2: 3: 3: 3: 3: 3: 3: 3: 3: 3: 3: 3: 3: 3:	SPTREMBL 25:* : sp_archea:* : sp_lung:* : sp_lung:* : sp_lung:* : sp_lung:* : sp_lung:* : sp_lunertebrate:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	096814 mus musculu Q7tmt6 mus musculu Q91441 mus musculu Q99104 mus musculu Q92440 mus musculu Q81712 mus musculu Q84000000000000000000000000000000000000
SUMMARIES ID	0998614 0717416 092401 092400 0917471 087.772 0800000 092447 092448 092483 092483
DB	: :
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		ŝ	œ	11	Q8K0Z4	Snw	mnscnjn
	462	5	4	11	Q924R0	mus	musculu
	461	75.1	m	11	Q924R6	mus	musculu
	461	2	4	11	092406	mus	musculu
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	460	74.9	4	11	Q924Q5	mus	musculu
	460	4.	4	11	Q91V67	នការ	musculu
	460	4.	4	11	092409	mus	musculu
		4.	-	11	Q9QXF0	mus	musculu
	458.5	4.	4	11	Q924Q3	mus	musculu
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	457.5	74.5	4	11	Q924R2	mus	musculu
	457	4.	ч	11	Q9Z1C4	mus	musculu
	457	4.	4	11	Q924R4	Enm	musculu
	456	4	481	11	Q8VCV5	mus	musculu
	453.5	ო	-	11	O9QXE9	BUM	musculu
	53.	ë.	4	11	Q924P5	ສກພ	musculu
	453	ω.	7	11	Q99L25	mns	musculu
	ഗ	ω.	143	11	Q924R7	anm	musculu
	449		109	11	Q9JL75	mus	musculu
	4	ω.	4	11	Q924P9	шnв	musculu
	•	m	120	11	Q920E8	mus	musculu
	4	ς,	4	11	Q91VA2	mus	musculu
	46.	ς.	9	11	Q8VDC9	BUM	musculu
	445.5	72.6	123	11	Q8VIJ1	Q8vij1 mus m	musculu
	4	72.5	œ	11	Q91WR1	mns	musculu
	4	ά.	m	11	Q7TPE3	Snu	musculu
	438	71.3	143	11	Q924P6	mus	musculu

ALIGNMENTS

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Strausberg R.;
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KRAIN-C57BL/GNCT; TISSUE=Hematopoietic Stem Cell;

KRAIN-C57BL/GNCT; PubMed=12477932;

RA Strausberg R.D., Felngold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaddo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Nodin T.B., Toethywis S., Carninci P., Prange C.,

RA Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

RA Rha S.S., Worley N.M., Sodergren R.J., Lu X., Glubs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glubs R.A.,

Rahes, J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M. M., Madan J.W., Schwuchenko Y., Boulfard G.G.,

RA Hakes, P.R., Touchman J.W., Green E.D., Dickson M.C.,

Ray Minishki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Gones Z.J., Marra M.A.,

R. Green E. Dickson M. Schonenene M., Madan A., Schein J.E.,

R. Gones S.J., Marra M.A.,

R. Green E.J., Marra M.A.,

R. Green E.J., Schnerch A., Schein J.E.,

R. Greenstein and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGGLEWIGKIGPGSGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQQSGABLVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                          DB 11; Length 473;
                                                                                                                                                                                                                                                                                       Score 526.5; DB 11; Length
Pred. No. 2.5e-46;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BC053409; AAH53409.1; -- Hypothetical protein.
                   MGD; MGI:96443; Igh-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
SWART; SW00406; IGv.
PROSITE; PS00289; IG_LIKE; 4.
PROSITE; PS00280; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW; 9DED57AS14475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               614 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                          85.7%;
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.9
Matches 101, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
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Best Local Similarity 79.8
Matches 95; Conservative
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1 QVQLQQSGABLURPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
                         20 QVQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRVYPGDGDTNY 79
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                                                                                                                                   80 NGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDYGSSYRFAYMGQGTLVTVSA 138
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                                                                                                      61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB069913; BAB61929.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
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01-JJM-2001 (TrEMBLrel. 17, Created)
01-JJM-2001 (TrEMBLrel. 17, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                         Q924Q1,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
V23-D-J-C mu protein (Fragment).
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                                                                                                                                                                                                                                                                                                  142
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PIR, F128833, F128833.
PIR, PH1156, PH1156.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SMART, SM00406; IGv: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mouse)
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NON TER
SEQUENCE
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481 AA

PRT;

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PRELIMINARY;
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Q8K172
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRTGQGLEWVGEIYPGSGNTYY 79
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                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CSTBL/6;
STRAIN=CSTBL/6;
Cxcno Y., Koznon H., Azuma T.;
Cxcno Y., Koznon H., Cxcno H., Cxcno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                  Query Match 77.7%; Score 477; DB 11; Length 463; Best Local Similarity 77.5%; Pred. No. 3.5e-41; Matches 93; Conservative 7; Mismatches 16; Indels '
              (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 78.0°
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE
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RESULT Q91WT1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLLQSGPELVKPGASVKISCKASGYTFTSYYIHWVKQRPGQGLVWIGWIYPGDGNTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus MCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                TISSUB-colon;
Strausberg R.;
Stubmitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0134990; AAH13490.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig-W.
Fran, PF0041; ig, 4.
SWART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
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QRK172,
QRK17
                                                                     Last sequence update)
Last annotation update)
                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Q91WT1;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2002) to the
EMBL; BC028249; AAH28249.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.4%
Best Local Similarity 91; Conservative
                                                                                                                                        Hypothetical protein.
Mus musculus (Mouse)
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TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Mus musculus (Mouse)
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NON TER
SEQUENCE
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Best Local S:
Matches 93
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                                                 Q924P7
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    RESULT 9
Q924P7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 NEKFKDKATLTADKSSTTVYMDLSRLISEDSAVYFCARHEDRGNYDGSLAWFVYWGQGTL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 NEKFKSKATLIVUDKPSSTAYMQLSSLTSEDSAVYYCTREGDYDAMDYWGQGTSVIVSS 137
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                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                        76.7%; Score 471; DB 11; Length 482; 76.3%; Pred. No. 1.6e-40; ive 11; Mismatches 15; Indels
PIR; PH1152; PH1152.

PIR; PH1153; PH1153.

InterPro: IPR00701359; Ig_cl.

InterPro: IPR003596; Ig_WC.

InterPro: IPR003596; Ig_WC.

InterPro: IPR003596; Ig_W.

InterPro: IPR00407; Igf. 4.

SMART; SM00407; Igf. 4.

SMART; SM00406; IGV; 1.

PROSITE; PS02939; IG_LKE; 4.

PROSITE; PS02939; IG_LKE; 4.

SRQUENCE 482 AA; $\frac{5}{2}$121 MW; A06FF0835771D084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Colon;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO183222; AAH18322.1; --
MGD; MGI:96486; Igh-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 AA
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01-MAR-2002 (TrEMBLrel. 20, C;
01-MAR-2002 (TrEMBLrel. 20, L;
01-OCT-2003 (TrEMBLrel. 25, L;
Hypothetical protein.
IGH-VJ558 OR AI893585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
Pfam; PF00047; Ig: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMARH; SM00406; 120; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.33
Marches 90, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 72.8
hes 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Matches
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Q8VCX4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP)."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TAXID=10090;
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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15988 MW; FB73958704796C9A CRC64;
                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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    PRT;
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PIR, F33932, F33932

PIR, PH1105, PH1105, PH1105, PH1105, PH1106, PH1106
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PROSITE; PS50835; IG_LIKE; 1.
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PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE
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Q924R3
ID Q924R
AC Q924R
DT 01-DE
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Q924P8
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SORRERS
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                                                                                                                                                                                                                                                                                             61 NEKFKGKATLITADKSSSTAYMQLSSLITSDDSAVYFCARD-GPW-FAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                          80 NEKFKGKATFTADTSSNIAYMQLSSLISEDSAVYYCARRLGRWYFDVWGAGTTVTVSS 137
                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.,
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067796; BAB63281.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                   Length 613;
       SEQUENCE FROM N.A.

TISSUB-Salivary gland;
Strausbear R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC01815; AAH18315.1; -
N MD; MCI: 96448; Igh-6.
InterPro; IPR003006; Igh-HC.
InterPro; IPR003006; Igh-HC.
InterPro; IPR003006; Igh-NC.
InterPro; IPR00406; Igh-V.
Ffam; PF00406; Igh-V.
ROSITE; PS00290; IGh-MHC; 3.
RPNOSITE; PS00290; IGH-MHC; 3.
RHYPOLABELCAL DATACELIN.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                          15; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                 76.2%; Score 468; DB 11; 77.1%; Pred. No. 4.3e-40; iive 10; Mismatches 15;
                                                                                                                                                                                                   Query Match
Best Local Similarity 77.18
Matches 91; Conservative
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PIR, PH1105, PH1105.
PIR, PH1114, PH11106.
PIR, PH1119, PH11119.
PIR, PH1125, PH1125.
PIR, PH1125, PH1126.
PIR, PH1129, PH1126.
PIR, PH1129, PH1126.
PIR, PH1129, PH1126.
PIR, PH1131, PH1131.
PIR, PH1134, PH1131.
PIR, PH1134, PH1134.
PIR, PH1134, PH1142.
PIR, PH1144, PH1142.
PIR, PH1144, PH1144.
PIR, PH1144, PH1144.
PIR, PH1149, PH1149.
PIR, PH1149, PH1149.
PIR, PH1150, PH1151.
PIR, PH1151, PH1151.
PIR, PH1152, PH1151.
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Q924Q4;
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Q924Q4
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KACADO Y., KACADO H., Azuma T.;

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3 witrophenyl) Acetyl (NP).";

KUMILL AB06917; BAB6393.1; -.

REL; AB06917; 128833.

RIS PRIN56; PRIN56;

RIS PRIN56; PRIN56;

RIS PRIN56; PRIN56;

REL REPROVILO; 19-1ike.

REPROVILO; 19-1ike.

REPROVILO; 10-1ike.

REPROVILOR REPROVILOR IN 10-1ike.

REPROVILOR REPROVIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVOLOQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NEKFKSKATLITVDKPSSTAYMQLSSLITSEDSAVYYCARDDYGRTFWGQGTTLTVSS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Best Local Similarity 76.0%; Score 466.5; DB 11; Length 140;
Best Local Similarity 76.9%; Pred. No. 9.5e-41;
Matches 90; Conservative 10; Mismatches 14; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
76.1%; Score 467; DB 11; Length 1
Best Local Similarity 75.9%; Pred. No. 8.5e-41;
Matches 88; Conservative 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                               141 141
141 AA; 15561 MW; DDD80482D66B76A0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
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V23-D-J-C MU.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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NCBI_TaxID=10090;
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NON TER
SEQUENCE
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Best Local &
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Q924R1;
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                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitropheny)] Acetyl (RP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067787; BAB63272.1; -.
                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 145
145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment)
Mus musculus (Mouse).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGv; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 75.8
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F28833.
PH1105.
PH1108.
PH1114.
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PH1153; PH1153.
S26744; S26744.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                             NCBI_TaxID=10090;
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PIR, PH1105, P
PIR, PH1114, P
PIR, PH1119, P
PIR, PH1129, P
PIR, PH1129, P
PIR, PH1129, P
PIR, PH1131, P
PIR, PH1131, P
PIR, PH1134, P
PIR, PH1134, P
PIR, PH1134, P
PIR, PH1142, P
PIR, PH1144, P
PIR, PH1144, P
PIR, PH1150, P
PIR, PH1150, P
PIR, PH1151, P
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SEQUENCE
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092407
1D 09240
AC 09240
DT 01-DE
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DT 01-DE
OC MAMM M
OC MAMM M
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Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"finity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067793; BAB63278.1;
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Kozono H., Azuma T.;
Kozono H., Azuma T.;
Spiret Beination of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).",
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 145;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PIR, PH1108, PH1108.

PIR, PH1109, PH1108.

PIR, PH1119, PH1119.

PIR, PH1119, PH1119.

PIR, PH1129, PH1126.

PIR, PH1126, PH126.

PIR, PH1126, PH126.

PIR, PH1127, PH128.

PIR, PH1131, PH131.

PIR, PH1131, PH131.

PIR, PH1134, PH134.

PIR, PH1134, PH134.

PIR, PH1134, PH1134.

PIR, PH1134, PH1136.

PIR, PH1142, PH1142.

PIR, PH1142, PH1142.

PIR, PH1142, PH1142.

PIR, PH1143, PH1143.

PIR, PH1143, PH1143.

PIR, PH1152, PH1153.

PIR, PH1153, PH1153.

PRAMMAN PRAMMAN PH1153.

PRAMM
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PROSITE; PS50835; IG_LIKE; 1.
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DR EMBL, AB067789; BAB63274.1; -.

DR PIR, PR3332; P33932.

DR PIR, PH105; PH1105.

DR PIR, PH1105; PH1106.

DR PIR, PH1105; PH1105.

DR PIR, PH1129; PH1128.

DR PIR, PH1129; PH1128.

DR PIR, PH1129; PH1128.

DR PIR, PH1139; PH1131.

DR PIR, PH1139; PH1139.

DR PIR, PH1139; PH139; PH139;
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Search completed: August 16, 2004, 11:10:29 Job time : 36.3318 secs

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